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(54) Title: NOVEL COMPOUNDS

(57) Abstract

This invention relates to newly identified polynucleotides, polypeptides encoded by such polynucleotides, the uses of such polynucleotides and polypeptides, as well as the production of such polynucleotides and polypeptides and recombinant host cells transformed with the polynucleotides. This invention also relates to inhibiting the biosynthesis or action of such polynucleotides or polypeptides and to the use of such inhibitors in therapy.

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NOVEL COMPOUNDS

Field of the Invention:

This invention relates to newly identified polynucleotides, polypeptides encoded by such polynucleotides, the uses of such polynucleotides and polypeptides, as well as the

- 5 production of such polynucleotides and polypeptides and recombinant host cells transformed with the polynucleotides. This invention also relates to inhibiting the biosynthesis or action of such polynucleotides or polypeptides and to the use of such inhibitors in therapy. Preferred embodiments of the invention include Streptococcal polypeptides and polynucleotides, particularly those of *Streptococcus pneumoniae*.

10 Background of the Invention:

The Streptococci make up a medically important genera of microbes known to cause several types of disease in humans, including otitis media, pneumonia and meningitis.

Since its isolation more than 100 years ago, *Streptococcus pneumoniae* has been one of the more intensively studied microbes. For example, much of our early understanding that

- 15 DNA is, in fact, the genetic material was predicated on the work of Griffith and of Avery, Macleod and McCarty using this microbe. Despite the vast amount of research with *S. pneumoniae*, many questions concerning the virulence of this microbe remain.

While certain Streptococcal factors associated with pathogenicity have been identified, e.g., capsule polysaccharides, peptidoglycans, pneumolysins, PspA Complement

- 20 factor H binding component, autolysin, neuraminidase, peptide permeases, hydrogen peroxide, IgA1 protease, the list is certainly not complete. Further very little is known concerning the temporal expression of such genes during infection and disease progression in a mammalian host. Discovering the sets of genes the bacterium is likely to be expressing at the different stages of infection, particularly when an infection is established, provides
- 25 critical information for the screening and characterization of novel antibacterials which can interrupt pathogenesis. In addition to providing a fuller understanding of known proteins, such an approach will identify previously unrecognised targets.

Brief Description of the Invention:

- 30 This invention provides novel proteins, particularly those from *Streptococcus pneumoniae*, strain 0100993, characterised in that it comprises the amino acid sequences given herein or fragments, analogues or derivatives thereof.

In accordance with another aspect of the present invention, there are provided polynucleotides (DNA or RNA) which encode such polypeptides.

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In particular the invention provides polynucleotides having the DNA sequences given herein.

The invention also relates to novel oligonucleotides derived from the sequences given herein which can act as PCR primers in the process herein described to determine whether or not the *Streptococcus pneumoniae* gene identified herein in whole or in part is expressed in infected tissue. It is recognised that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained. The proteins so identified are also useful as targets in screens designed to identify antimicrobial compounds.

10 It is an object of the invention to provide polypeptides that have been identified as novel polypeptides by homology between the amino acid sequence set out in the Sequence Listing and a known amino acid sequence or sequences of other proteins such as the proteins identified under the heading Identity in Table 1.

15 It is a further object of the invention to provide polynucleotides that encode polypeptides set forth in the Sequence Listing, particularly polynucleotides that encode the polypeptide set forth in the Sequence Listing.

In a particularly preferred embodiment of the invention the polynucleotide comprises a region encoding polypeptides comprising the sequence set out in the Sequence Listing, or a variant thereof.

20 In another particularly preferred embodiment of the invention there is a novel protein from comprising an amino acid sequence of the Sequence Listing, or a variant thereof.

25 In accordance with another aspect of the invention, there is provided the use of a polynucleotide of the invention for therapeutic or prophylactic purposes, in particular genetic immunization. Among the particularly preferred embodiments of the invention are naturally occurring allelic variants the polynucleotides set forth in the Sequence Listing and polypeptides encoded thereby.

In accordance with yet another aspect of the invention, there are provided inhibitors to such polypeptides, useful as antibacterial agents, including, for example, antibodies.

30 In accordance with certain preferred embodiments of the invention, there are provided products, compositions and methods for assessing expression of the sequences the Sequence Listing, treating disease, for example, otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema and endocarditis, and most particularly meningitis, such as for example infection of cerebrospinal fluid, assaying genetic variation, and

administering a polypeptide or polynucleotide of the invention to an organism to raise an immunological response against a bacteria, especially a *Streptococcus pneumoniae* bacteria.

In accordance with certain preferred embodiments of this and other aspects of the invention there are provided polynucleotides that hybridize to polynucleotide sequences of the invention, particularly under stringent conditions.

5 In certain preferred embodiments of the invention there are provided antibodies against polypeptides of the invention.

In other embodiments of the invention there are provided methods for identifying compounds which bind to or otherwise interact with and inhibit or activate an activity of a 10 polypeptide or polynucleotide of the invention comprising: contacting a polypeptide or polynucleotide of the invention with a compound to be screened under conditions to permit binding to or other interaction between the compound and the polypeptide or polynucleotide to assess the binding to or other interaction with the compound, such binding or interaction being associated with a second component capable of providing a detectable signal in response to the 15 binding or interaction of the polypeptide or polynucleotide with the compound; and determining whether the compound binds to or otherwise interacts with and activates or inhibits an activity of the polypeptide or polynucleotide by detecting the presence or absence of a signal generated from the binding or interaction of the compound with the polypeptide or polynucleotide.

In accordance with yet another aspect of the invention, there are provided agonists and 20 antagonists of the polynucleotide and/or polypeptides of the invention, preferably bacteriostatic or bacteriocidal agonists and antagonists.

In a further aspect of the invention there are provided compositions comprising a polynucleotide or a polypeptide of the invention for administration to a cell or to a multicellular organism.

25 Various changes and modifications within the spirit and scope of the disclosed invention will become readily apparent to those skilled in the art from reading the following descriptions and from reading the other parts of the present disclosure.

Detailed Description of the Invention:

Each of the DNA sequences provided herein may be used in the discovery and 30 development of antibacterial compounds. Because each of the sequences contains an open reading frame (ORF) with appropriate initiation and termination codons, the encoded protein upon expression can be used as a target for the screening of antimicrobial drugs. Additionally, the DNA sequences encoding preferably the amino terminal regions of the encoded protein or the Shine-Delgarno region can be used to construct antisense sequences

to control the expression of the coding sequence of interest. Furthermore, many of the sequences disclosed herein also provide regions upstream and downstream from the encoding sequence. These sequences are useful as a source of regulatory elements for the control of bacterial gene expression. Such sequences are conveniently isolated by 5 restriction enzyme action or synthesized chemically and introduced, for example, into promoter identification strains. These strains contain a reporter structural gene sequence located downstream from a restriction site such that if an active promoter is inserted, the reporter gene will be expressed.

Although each of the sequences may be employed as described above, this 10 invention also provides several means for identifying particularly useful target genes. The first of these approaches entails searching appropriate databases for sequence matches in related organisms. Thus, if a homologue exists, the Streptococcal-like form of this gene would likely play an analogous role. For example, a Streptococcal protein identified as homologous to a cell surface protein in another organism would be useful as a vaccine 15 candidate. To the extent such homologies have been identified for the sequences disclosed herein they are reported along with the encoding sequence.

Recently techniques have become available to evaluate temporal gene expression in bacteria, particularly as it applies to viability under laboratory and infection conditions. A number of methods can be used to identify genes which are essential to survival *per se*, or 20 essential to the establishment/maintenance of an infection. Identification of an ORF unknown by one of these methods yields additional information about its function and permits the selection of such an ORF for further development as a screening target. Briefly, these approaches include:

1) Signature Tagged Mutagenesis (STM)

25 This technique is described by Hensel et al., *Science* 269: 400-403(1995), the contents of which is incorporated by reference for background purposes. Signature tagged mutagenesis identifies genes necessary for the establishment/maintenance of infection in a given infection model.

The basis of the technique is the random mutagenesis of target organism by various 30 means (e.g., transposons) such that unique DNA sequence tags are inserted in close proximity to the site of mutation. The tags from a mixed population of bacterial mutants and bacteria recovered from an infected hosts are detected by amplification, radiolabeling and hybridisation analysis. Mutants attenuated in virulence are revealed by absence of the tag from the pool of bacteria recovered from infected hosts.

In *Streptococcus pneumoniae*, because the transposon system is less well developed, a more efficient way of creating the tagged mutants is to use the insertion-duplication mutagenesis technique as described by Morrison et al., *J. Bacteriol.* 159:870 (1984) the contents of which is incorporated by reference for background purposes.

5 **2) In Vivo Expression Technology (IVET)**

This technique is described by Camilli et al., *Proc. Nat'l. Acad. Sci. USA*. 91:2634-2638 (1994), the contents of which is incorporated by reference for background purposes. IVET identifies genes up-regulated during infection when compared to laboratory cultivation, implying an important role in infection. ORF identified by this technique are implied to have a significant role in infection establishment/maintenance.

10 In this technique random chromosomal fragments of target organism are cloned upstream of a promoter-less recombinase gene in a plasmid vector. This construct is introduced into the target organism which carries an antibiotic resistance gene flanked by resolvase sites. Growth in the presence of the antibiotic removes from the population those 15 fragments cloned into the plasmid vector capable of supporting transcription of the recombinase gene and therefore have caused loss of antibiotic resistance. The resistant pool is introduced into a host and at various times after infection bacteria may be recovered and assessed for the presence of antibiotic resistance. The chromosomal fragment carried by each antibiotic sensitive bacterium should carry a promoter or portion of a gene normally 20 upregulated during infection. Sequencing upstream of the recombinase gene allows identification of the up regulated gene.

25 **3) Differential display**

This technique is described by Chuang et al., *J. Bacteriol.* 175:2026-2036 (1993), the contents of which is incorporated by reference for background purposes. This method identifies those genes which are expressed in an organism by identifying mRNA present using randomly-primed RT-PCR. By comparing pre-infection and post infection profiles, genes up and down regulated during infection can be identified and the RT-PCR product sequenced and matched to ORF 'unknowns'.

4) Generation of conditional lethal mutants by transposon mutagenesis.

This technique, described by de Lorenzo, V. et al., *Gene* 123:17-24 (1993); Neuwald, A. F. et al., *Gene* 125: 69-73(1993); and Takiff, H. E. et al., *J. Bacteriol.* 174:1544-1553(1992), the contents of which is incorporated by reference for

- 5 background purposes, identifies genes whose expression are essential for cell viability.

In this technique transposons carrying controllable promoters, which provide transcription outward from the transposon in one or both directions, are generated. Random insertion of these transposons into target organisms and subsequent isolation of insertion mutants in the presence of inducer of promoter activity ensures that insertions which
10 separate promoter from coding region of a gene whose expression is essential for cell viability will be recovered. Subsequent replica plating in the absence of inducer identifies such insertions, since they fail to survive. Sequencing of the flanking regions of the transposon allows identification of site of insertion and identification of the gene disrupted. Close monitoring of the changes in cellular processes/morphology during growth in the
15 absence of inducer yields information on likely function of the gene. Such monitoring could include flow cytometry (cell division, lysis, redox potential, DNA replication), incorporation of radiochemically labeled precursors into DNA, RNA, protein, lipid, peptidoglycan, monitoring reporter enzyme gene fusions which respond to known cellular stresses.

20 **5) Generation of conditional lethal mutants by chemical mutagenesis.**

This technique is described by Beckwith, J., *Methods in Enzymology* 204: 3-18(1991), the contents of which are incorporated herein by reference for background purposes. In this technique random chemical mutagenesis of target organism, growth at temperature other than physiological temperature (permissive temperature) and subsequent
25 replica plating and growth at different temperature (e.g. 42°C to identify ts, 25°C to identify cs) are used to identify those isolates which now fail to grow (conditional mutants). As above close monitoring of the changes upon growth at the non-permissive temperature yields information on the function of the mutated gene. Complementation of conditional lethal mutation by library from target organism and sequencing of complementing gene
30 allows matching with unknown ORF.

6) RT-PCR

Streptococcus pneumoniae messenger RNA is isolated from bacterial infected tissue e.g. 48 hour murine lung infections, and the amount of each mRNA species assessed by reverse transcription of the RNA sample primed with random hexanucleotides followed by PCR

with gene specific primer pairs. The determination of the presence and amount of a particular mRNA species by quantification of the resultant PCR product provides information on the bacterial genes which are transcribed in the infected tissue. Analysis of gene transcription can be carried out at different times of infection to gain a detailed

5 knowledge of gene regulation in bacterial pathogenesis allowing for a clearer understanding of which gene products represent targets for screens for novel antibacterials. Because of the gene specific nature of the PCR primers employed it should be understood that the bacterial mRNA preparation need not be free of mammalian RNA. This allows the investigator to carry out a simple and quick RNA preparation from infected tissue to

10 obtain bacterial mRNA species which are very short lived in the bacterium (in the order of 2 minute halflives). Optimally the bacterial mRNA is prepared from infected murine lung tissue by mechanical disruption in the presence of TRIzole (GIBCO-BRL) for very short periods of time, subsequent processing according to the manufacturers of TRIzole reagent and DNAase treatment to remove contaminating DNA. Preferably the process is optimised

15 by finding those conditions which give a maximum amount of *S.pneumoniae* 16S ribosomal RNA as detected by probing Northerns with a suitably labelled sequence specific oligonucleotide probe. Typically a 5' dye labelled primer is used in each PCR primer pair in a PCR reaction which is terminated optimally between 8 and 25 cycles. The PCR products are separated on 6% polyacrylamide gels with detection and quantification using

20 GeneScanner (manufactured by ABI).

Each of these techniques may have advantages or disadvantage depending on the particular application. The skilled artisan would choose the approach that is the most relevant with the particular end use in mind. For example, some genes might be recognised as essential for infection but in reality are only necessary for the initiation of infection and

25 so their products would represent relatively unattractive targets for antibacterials developed to cure established and chronic infections.

Use of the of these technologies when applied to the ORFs of the present invention enables identification of bacterial proteins expressed during infection, inhibitors of which would have utility in anti-bacterial therapy.

30 *Streptococcus pneumoniae*, strain 0100993 has been deposited at the National Collection of Industrial and Marine Bacteria Ltd. (NCIMB), Aberdeen, Scotland under NCIMB number 40794 on 11 April 1996, and a *Streptococcus pneumoniae*, strain 0100993 DNA library in *E. coli* was similarly deposited on 17 April 1996 under NCIMB number 40800.

The nucleotide sequences disclosed herein can be obtained by synthetic chemical techniques known in the art or can be obtained from *Streptococcus pneumoniae*, strain 0100993 by probing a DNA preparation with probes constructed from the particular sequences disclosed herein. Alternatively, oligonucleotides derived from a disclosed sequence can act as PCR primers in a process of PCR-based cloning of the sequence from a bacterial genomic source. It is recognised that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained.

To obtain the polynucleotide encoding the protein using the DNA sequence given herein typically a library of clones of chromosomal DNA of *Streptococcus pneumoniae*, strain 0100993 in *E. coli* or some other suitable host is probed with a radiolabelled oligonucleotide, preferably a 17mer or longer, derived from the partial sequence. Clones carrying DNA identical to that of the probe can then be distinguished using high stringency washes. By sequencing the individual clones thus identified with sequencing primers designed from the original sequence it is then possible to extend the sequence in both directions to determine the full gene sequence. Conveniently such sequencing is performed using denatured double stranded DNA prepared from a plasmid clone. Suitable techniques are described by Maniatis, T., Fritsch, E.F. and Sambrook, J. in MOLECULAR CLONING, A Laboratory Manual, 2nd edition, 1989, Cold Spring Harbor Laboratory (see: Screening By Hybridization 1.90 and Sequencing Denatured Double-Stranded DNA Templates 20 13.70).

A polynucleotide of the present invention may be in the form of RNA or in the form of DNA, which DNA includes cDNA, genomic DNA, and synthetic DNA. The DNA may be double-stranded or single-stranded, and if single stranded may be the coding strand or non-coding (anti-sense) strand. The coding sequence which encodes the polypeptide 25 may be identical to the coding sequence shown or may be a different coding sequence which coding sequence, as a result of the redundancy or degeneracy of the genetic code, encoding the same polypeptide.

The present invention includes variants of the hereinabove described polynucleotides which encode fragments, analogues and derivatives of the polypeptide 30 characterized by the deduced amino acid sequence given herein. The variant of the polynucleotide may be a naturally occurring allelic variant of the polynucleotide or a non-naturally occurring variant of the polynucleotide. In addition to the standard A, G, C, T/U representations for nucleic acid bases, the term "N" is also used. "N" means that any of the four DNA or RNA bases may appear at such a designated position in the DNA or RNA.

sequence, except that N cannot be a base that when taken in combination with adjacent nucleotide positions, when read in the correct reading frame, would have the effect of generating a premature termination codon in such reading frame.

- Thus, the present invention includes polynucleotides encoding the same
- 5 polypeptide characterized by the deduced amino acid sequence given herein as well as variants of such polynucleotides which variants encode for a fragment, derivative or analogue of the polypeptide. Such nucleotide variants include deletion variants, substitution variants and addition or insertion variants.

The polynucleotide may have a coding sequence which is a naturally occurring

10 allelic variant of the coding sequence characterized by the DNA sequence disclosed herein. As known in the art, an allelic variant is an alternate form of a polynucleotide sequence which may have a substitution, deletion or addition of one or more nucleotides, which does not substantially alter the function of the encoded polypeptide.

The polynucleotide which encodes for the mature polypeptide, may include only

15 the coding sequence for the mature polypeptide or the coding sequence for the mature polypeptide and additional coding sequence such as a leader or secretory sequence or a proprotein sequence.

Thus, the term "polynucleotide encoding a polypeptide" encompasses a polynucleotide which includes only coding sequence for the polypeptide as well as a

20 polynucleotide which includes additional coding and/or non-coding sequence.

The present invention therefore includes polynucleotides, wherein the coding sequence for the mature polypeptide may be fused in the same reading frame to a polynucleotide sequence which aids in expression and secretion of a polypeptide from a host cell, for example, a leader sequence which functions as a secretory sequence for

25 controlling transport of a polypeptide from the cell. The polypeptide having a leader sequence is a proprotein and may have the leader sequence cleaved by the host cell to form the mature form of the polypeptide. The polynucleotides may also encode for a proprotein which is the mature protein plus additional 5' amino acid residues. A mature protein having a prosequence is a proprotein and may be an inactive form of the protein. Once the

30 prosequence is cleaved an active mature protein remains.

Thus, for example, the polynucleotide of the present invention may code for a mature protein, or for a protein having a prosequence or for a protein having both a prosequence and a presequence (leader sequence). Further, the amino acid sequences provided herein show a methionine residue at the NH₂-terminus. It is appreciated, however,

that during post-translational modification of the peptide, this residue may be deleted.

Accordingly, this invention contemplates the use of both the methionine-containing and the methionineless amino terminal variants of each protein disclosed herein.

The polynucleotides of the present invention may also have the coding sequence

5 fused in frame to a marker sequence at either the 5' or 3' terminus of the gene which allows for purification of the polypeptide of the present invention. The marker sequence may be a hexa-histidine tag supplied by the pQE series of vectors (supplied commercially by Quiagen Inc.) to provide for purification of the polypeptide fused to the marker in the case of a bacterial host.

10 The present invention further relates to polynucleotides which hybridize to the hereinabove-described sequences if there is at least 50% and preferably at least 70% identity between the sequences. The present invention particularly relates to polynucleotides, particularly Streptococcal polynucleotides, which hybridize under stringent conditions to the hereinabove-described polynucleotides. As herein used, the term "stringent conditions"

15 means hybridization will occur only if there is at least 95% and preferably at least 97% identity between the sequences. The polynucleotides which hybridize to the hereinabove described polynucleotides in a preferred embodiment encode polypeptides which retain substantially the same biological function or activity as the polypeptide characterised by the deduced amino acid sequence given herein. An example of stringent hybridization

20 conditions is overnight incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 micrograms/ml denatured, sheared salmon sperm DNA, followed by washing the hybridization support in 0.1x SSC at about 65°C.

Hybridization and wash conditions are well known and exemplified in Sambrook, *et al.*, Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, N.Y., (1989), particularly Chapter 11 therein.

25 The invention also provides a polynucleotide consisting essentially of a polynucleotide sequence obtainable by screening an appropriate library containing the complete gene for a polynucleotide sequence selected from the group consisting of the 30 polynucleotides of the Sequence Listing under stringent hybridization conditions with a probe having the sequence of said polynucleotide sequence set forth in said polynucleotide of the Sequence Listing or a fragment thereof; and isolating said DNA sequence. Fragments useful for obtaining such a polynucleotide include, for example, probes and primers described elsewhere herein.

"Identity," as known in the art and used herein, is a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match 5 between strings of such sequences. "Identity" and "similarity" can be readily calculated by known methods, including but not limited to those described in (*Computational Molecular Biology*, Lesk, A.M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D.W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data*, Part I, Griffin, A.M., and Griffin, H.G., eds., 10 Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; and Carillo, H., and Lipman, D., *SIAM J. Applied Math.*, 48: 1073 (1988). Preferred methods to determine identity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity 15 are codified in publicly available computer programs. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, the GCG program package (Devereux, J., et al., *Nucleic Acids Research* 12(1): 387 (1984)), BLASTP, BLASTN, and FASTA (Atschul, S.F. et al., *J. Molec. Biol.* 215: 403-410 (1990). The BLAST X program is publicly available from NCBI and other sources (*BLAST 20 Manual*, Altschul, S., et al., NCBI NLM NIH Bethesda, MD 20894; Altschul, S., et al., *J. Mol. Biol.* 215: 403-410 (1990).

As an illustration, by a polynucleotide having a nucleotide sequence having at least, for example, 95% "identity" to a reference nucleotide sequence selected from the group consisting of the polynucleotide of the Sequence Listing is intended that the nucleotide 25 sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another 30 nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. These mutations of the reference sequence may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among

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nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence.

Similarly, by a polypeptide having an amino acid sequence having at least, for example, 95% identity to a reference amino acid sequence of selected from the group consisting of the amino acids of the Sequence Listing is intended that the amino acid sequence of the polypeptide is identical to the reference sequence except that the polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the reference amino acid. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a reference amino acid sequence, up to 5% of the amino acid residues in the reference sequence may be deleted or substituted with another amino acid, or a number of amino acids up to 5% of the total amino acid residues in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

The deposit referred to herein will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Micro-organisms for purposes of Patent Procedure. These deposits are provided merely as convenience to those of skill in the art and are not an admission that a deposit is required under 35 U.S.C. §112. The sequence of the polynucleotides contained in the deposited material, as well as the amino acid sequence of the polypeptides encoded thereby, are incorporated herein by reference and are controlling in the event of any conflict with any description of sequences herein. A license may be required to make, use or sell the deposited material, and no such license is hereby granted.

The terms "fragment," "derivative" and "analogue" when referring to the polypeptide characterized by the deduced amino acid sequence herein, means a polypeptide which retains essentially the same biological function or activity as such polypeptide. Thus, an analogue includes a proprotein which can be activated by cleavage of the proprotein portion to produce an active mature polypeptide.

The polypeptide of the present invention may be a recombinant polypeptide, a natural polypeptide or a synthetic polypeptide, preferably a recombinant polypeptide.

The fragment, derivative or analogue of the polypeptide characterized by the deduced amino acid sequence herein may be (i) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be 5 one encoded by the genetic code, or (ii) one in which one or more of the amino acid residues includes a substituent group, or (iii) one in which the polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol), or (iv) one in which the additional amino acids are fused to the polypeptide, such as a leader or secretory sequence or a sequence which is employed for 10 purification of the polypeptide or a proprotein sequence. Such fragments, derivatives and analogues are deemed to be within the scope of those skilled in the art from the teachings herein.

The polypeptides and polynucleotides of the present invention are preferably provided in an isolated form, and preferably are purified to homogeneity.

15 The term "isolated" means that the material is removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or polypeptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotides could be part of a vector 20 and/or such polynucleotides or polypeptides could be part of a composition, and still be isolated in that such vector or composition is not part of its natural environment.

The present invention also relates to vectors which include polynucleotides of the present invention, host cells which are genetically engineered with vectors of the invention and the production of polypeptides of the invention by recombinant techniques.

25 In accordance with yet a further aspect of the present invention, there is therefore provided a process for producing the polypeptide of the invention by recombinant techniques by expressing a polynucleotide encoding said polypeptide in a host and recovering the expressed product. Alternatively, the polypeptides of the invention can be synthetically produced by conventional peptide synthesizers.

30 Host cells are genetically engineered (transduced or transformed or transfected) with the vectors of this invention which may be, for example, a cloning vector or an expression vector. The vector may be, for example, in the form of a plasmid, a cosmid, a phage, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the

genes. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

Suitable expression vectors include chromosomal, nonchromosomal and synthetic

- 5 DNA sequences, e.g., bacterial plasmids; phage DNA; baculovirus; yeast plasmids; vectors derived from combinations of plasmids and phage DNA. However, any other vector may be used as long as it is replicable and viable in the host.

- 10 The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is inserted into an appropriate restriction endonuclease site(s) by procedures known in the art.

- 15 The DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct mRNA synthesis. As representative examples of such promoters, there may be mentioned: LTR or SV40 promoter, the *E. coli lac* or *trp*, the phage lambda *P_L* promoter and other promoters known to control expression of genes in eukaryotic or prokaryotic cells or their viruses. The expression vector also contains a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression.

- 20 In addition, the expression vectors preferably contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in *E. coli*.

- 25 The gene can be placed under the control of a promoter, ribosome binding site (for bacterial expression) and, optionally, an operator (collectively referred to herein as "control elements), so that the DNA sequence encoding the desired protein is transcribed into RNA in the host cell transformed by a vector containing this expression construction. The coding sequence may or may not contain a signal peptide or leader sequence. The polypeptides of the present invention can be expressed using, for example, the *E. coli* tac promoter or the protein A gene (spa) promoter and signal sequence. Leader sequences can be removed by the bacterial host in post-translational processing. See, e.g., U.S. Patent Nos. 4,431,739; 30 4,425,437; 4,338,397. Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are PKK232-8 and PCM7. Particular named bacterial promoters include *lacI*, *lacZ*, *T3*, *T7*, *gpt*, lambda *P_R*, *P_L* and *trp*. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and

mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

- In addition to control sequences, it may be desirable to add regulatory sequences which allow for regulation of the expression of the protein sequences relative to the growth
- 5 of the host cell. Regulatory sequences are known to those of skill in the art, and examples include those which cause the expression of a gene to be turned on or off in response to a chemical or physical stimulus, including the presence of a regulatory compound. Other types of regulatory elements may also be present in the vector, for example, enhancer sequences.
- 10 An expression vector is constructed so that the particular coding sequence is located in the vector with the appropriate regulatory sequences, the positioning and orientation of the coding sequence with respect to the control sequences being such that the coding sequence is transcribed under the "control" of the control sequences (i.e., RNA polymerase which binds to the DNA molecule at the control sequences transcribes the coding sequence). Modification of the coding sequences may be desirable to achieve this end. For example, in some cases it may be necessary to modify the sequence so that it may be attached to the control sequences with the appropriate orientation; i.e., to maintain the reading frame. The control sequences and other regulatory sequences may be ligated to the coding sequence prior to insertion into a vector, such as the cloning vectors described
- 15 above. Alternatively, the coding sequence can be cloned directly into an expression vector which already contains the control sequences and an appropriate restriction site.
- 20

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal

25 identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product.

30

The vector containing the appropriate DNA sequence as hereinabove described, as well as an appropriate promoter or control sequence, may be employed to transform an appropriate host to permit the host to express the protein.

- More particularly, the present invention also includes recombinant constructs comprising one or more of the sequences as broadly described above. The constructs comprise a vector, such as a plasmid or viral vector, into which a sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available. The following vectors are provided by way of example. Bacterial: pET-3 vectors (Stratagene), pQE70, pQE60, pQE-9 (Qiagen), pbs, pD10, phagescript, psiX174, pbluescript SK, pbsks, pNH8A, pNH16a, pNH18A, pNH46A (Stratagene); ptrc99a, pKK223-3, pKK233-3, pDR540, pRITS (Pharmacia). Eukaryotic: pBlueBacIII (Invitrogen), pWLNEO, pSV2CAT, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia). However, any other plasmid or vector may be used as long as they are replicable and viable in the host.
- Examples of recombinant DNA vectors for cloning and host cells which they can transform include the bacteriophage *l* (*E. coli*), pBR322 (*E. coli*), pACYC177 (*E. coli*), pKT230 (gram-negative bacteria), pGV1106 (gram-negative bacteria), pLAFR1 (gram-negative bacteria), pME290 (non-*E. coli* gram-negative bacteria), pHV14 (*E. coli* and *Bacillus subtilis*), pBD9 (*Bacillus*), pJ61 (*Streptomyces*), pUC6 (*Streptomyces*), YIp5 (*Saccharomyces*), a baculovirus insect cell system, YCp19 (*Saccharomyces*). See, generally, "DNA Cloning": Vols. I & II, Glover *et al.* ed. IRL Press Oxford (1985) (1987) and; T. Maniatis *et al.* ("Molecular Cloning" Cold Spring Harbor Laboratory (1982)).
- In some cases, it may be desirable to add sequences which cause the secretion of the polypeptide from the host organism, with subsequent cleavage of the secretory signal.
- Polypeptides can be expressed in host cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, *et al.*, Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, N.Y., (1989), the disclosure of which is hereby incorporated by reference.
- Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period.

Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents, such methods are well known to those skilled in the art.

Depending on the expression system and host selected, the polypeptide of the present invention may be produced by growing host cells transformed by an expression vector described above under conditions whereby the polypeptide of interest is expressed.

The polypeptide is then isolated from the host cells and purified. If the expression system

secretes the polypeptide into growth media, the polypeptide can be purified directly from the media. If the polypeptide is not secreted, it is isolated from cell lysates or recovered from the cell membrane fraction. Where the polypeptide is localized to the cell surface, whole cells or isolated membranes can be used as an assayable source of the desired gene product. Polypeptide expressed in bacterial hosts such as *E. coli* may require isolation from inclusion bodies and refolding. Where the mature protein has a very hydrophobic region which leads to an insoluble product of overexpression, it may be desirable to express a truncated protein in which the hydrophobic region has been deleted. The selection of the appropriate growth conditions and recovery methods are within the skill of the art.

The polypeptide can be recovered and purified from recombinant cell cultures by methods including ammonium sulphate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps.

Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. Polypeptides of the invention may also include an initial methionine amino acid residue.

A "replicon" is any genetic element (e.g., plasmid, chromosome, virus) that functions as an autonomous unit of DNA replication *in vivo*; i.e., capable of replication under its own control.

A "vector" is a replicon, such as a plasmid, phage, or cosmid, to which another DNA segment may be attached so as to bring about the replication of the attached segment.

A "double-stranded DNA molecule" refers to the polymeric form of deoxyribonucleotides (bases adenine, guanine, thymine, or cytosine) in a double-stranded helix, both relaxed and supercoiled. This term refers only to the primary and secondary structure of the molecule, and does not limit it to any particular tertiary forms. Thus, this 5 term includes double-stranded DNA found, *inter alia*, in linear DNA molecules (e.g., restriction fragments), viruses, plasmids, and chromosomes. In discussing the structure of particular double-stranded DNA molecules, sequences may be described herein according to the normal convention of giving only the sequence in the 5' to 3' direction along the nontranscribed strand of DNA (i.e., the strand having the sequence homologous to the 10 mRNA).

A DNA "coding sequence of" or a "nucleotide sequence encoding" a particular protein, is a DNA sequence which is transcribed and translated into a polypeptide when placed under the control of appropriate regulatory sequences.

A "promoter sequence" is a DNA regulatory region capable of binding RNA 15 polymerase in a cell and initiating transcription of a downstream (3' direction) coding sequence. For purposes of defining the present invention, the promoter sequence is bound at the 3' terminus by a translation start codon (e.g., ATG) of a coding sequence and extends upstream (5' direction) to include the minimum number of bases or elements necessary to initiate transcription at levels detectable above background. Within the promoter sequence 20 will be found a transcription initiation site (conveniently defined by mapping with nuclease S1), as well as protein binding domains (consensus sequences) responsible for the binding of RNA polymerase. Eukaryotic promoters will often, but not always, contain "TATA" boxes and "CAT" boxes. Prokaryotic promoters contain Shine-Dalgarno sequences in addition to the -10 and -35 consensus sequences.

DNA "control sequences" refers collectively to promoter sequences, ribosome 25 binding sites, polyadenylation signals, transcription termination sequences, upstream regulatory domains, enhancers, and the like, which collectively provide for the expression (i.e., the transcription and translation) of a coding sequence in a host cell.

A control sequence "directs the expression" of a coding sequence in a cell when 30 RNA polymerase will bind the promoter sequence and transcribe the coding sequence into mRNA, which is then translated into the polypeptide encoded by the coding sequence.

A "host cell" is a cell which has been transformed or transfected, or is capable of transformation or transfection by an exogenous DNA sequence.

A cell has been "transformed" by exogenous DNA when such exogenous DNA has been introduced inside the cell membrane. Exogenous DNA may or may not be integrated (covalently linked) into chromosomal DNA making up the genome of the cell. In prokaryotes and yeasts, for example, the exogenous DNA may be maintained on an

5 episomal element, such as a plasmid. With respect to eukaryotic cells, a stably transformed or transfected cell is one in which the exogenous DNA has become integrated into the chromosome so that it is inherited by daughter cells through chromosome replication. This stability is demonstrated by the ability of the eukaryotic cell to establish cell lines or clones comprised of a population of daughter cell containing the exogenous DNA.

10 A "clone" is a population of cells derived from a single cell or common ancestor by mitosis. A "cell line" is a clone of a primary cell that is capable of stable growth *in vitro* for many generations.

15 A "heterologous" region of a DNA construct is an identifiable segment of DNA within or attached to another DNA molecule that is not found in association with the other molecule in nature.

20 This invention is also related to the use of the polynucleotides of the invention for use as diagnostic reagents. Detection of a polynucleotide or polypeptide of the invention in a eukaryote, particularly a mammal, and especially a human, will provide a diagnostic method for diagnosis of a disease. Eukaryotes (herein also "individual(s)"), particularly mammals, and especially humans, infected with an organism comprising a polynucleotide of the invention may be detected at the nucleic acid level by a variety of techniques.

25 Nucleic acids for diagnosis may be obtained from an infected individual's cells and tissues, such as bone, blood, muscle, cartilage, and skin. Genomic DNA may be used directly for detection or may be amplified enzymatically by using PCR or other amplification technique prior to analysis. RNA or cDNA may also be used in the same ways. Using amplification, characterization of the species and strain of prokaryote present in an individual, may be made by an analysis of the genotype of the prokaryote gene. Deletions and insertions can be detected by a change in size of the amplified product in comparison to the genotype of a reference sequence. Point mutations can be identified by hybridizing amplified DNA to labeled polynucleotide sequences of the invention. Perfectly matched sequences can be distinguished from mismatched duplexes by RNase digestion or by differences in melting temperatures. DNA sequence differences may also be detected by alterations in the electrophoretic mobility of the DNA fragments in gels, with or without denaturing agents, or by direct DNA sequencing. See, e.g., Myers et al., *Science*, 230: 1242 (1985). Sequence changes at specific locations also may be

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revealed by nuclease protection assays, such as RNase and S1 protection or a chemical cleavage method. See, e.g., Cotton et al., *Proc. Natl. Acad. Sci. USA*, 85: 4397-4401 (1988).

Cells carrying mutations or polymorphisms in the gene of the invention may also be detected at the DNA level by a variety of techniques, to allow for serotyping, for example. For example, RT-PCR can be used to detect mutations. It is particularly preferred to use RT-PCR in conjunction with automated detection systems, such as, for example, GeneScan. RNA or cDNA may also be used for the same purpose, PCR or RT-PCR. As an example, PCR primers complementary to a nucleic acid encoding a polypeptide of the invention can be used to identify and analyze mutations. These primers may be used for, among other things, amplifying DNA isolated from a sample derived from an individual. The primers may be used to amplify the gene isolated from an infected individual such that the gene may then be subject to various techniques for elucidation of the DNA sequence. In this way, mutations in the DNA sequence may be detected and used to diagnose infection and to serotype and/or classify the infectious agent.

The invention further provides a process for diagnosing disease, preferably bacterial infections, more preferably infections by *Streptococcus pneumoniae*, comprising determining from a sample derived from an individual a increased level of expression of polynucleotide having a sequence set forth in the Sequence Listing or a sequence of the invention. Increased or decreased expression of a polynucleotide of the invention can be measured using any one of the methods well known in the art for the quantitation of polynucleotides, such as, for example, amplification, PCR, RT-PCR, RNase protection, Northern blotting and other hybridization methods.

In addition, a diagnostic assay in accordance with the invention for detecting over-expression of a polypeptide of the invention compared to normal control tissue samples may be used to detect the presence of an infection, for example. Assay techniques that can be used to determine levels of a polypeptide of the invention, in a sample derived from a host are well-known to those of skill in the art. Such assay methods include radioimmunoassays, competitive-binding assays, Western Blot analysis and ELISA assays.

In accordance with yet a further aspect of the present invention, there is provided the use of a polypeptide of the invention for therapeutic or prophylactic purposes, for example, as an antibacterial agent or a vaccine.

In accordance with another aspect of the present invention, there is provided the use of a polynucleotide of the invention for therapeutic or prophylactic purposes, in particular genetic immunisation.

In accordance with yet another aspect of the present invention, there are provided inhibitors to such polypeptides, useful as antibacterial agents. In particular, there are provided antibodies against such polypeptides.

Polypeptides of the invention may also be used to assess the binding of small molecule substrates and ligands in, for example, cells, cell-free preparations, chemical libraries, and natural product mixtures. These substrates and ligands may be natural substrates and ligands or may be structural or functional mimetics. See, e.g., Coligan *et al.*, *Current Protocols in Immunology* 1(2): Chapter 5 (1991).

The invention also provides a method of screening compounds to identify those which enhance (agonist) or block (antagonist) the action of polypeptides or polynucleotides of the invention, particularly those compounds that are bacteriostatic and/or bacteriocidal. The method of screening may involve high-throughput techniques. For example, to screen for agonists or antagonists, a synthetic reaction mix, a cellular compartment, such as a membrane, cell envelope or cell wall, or a preparation of any thereof, comprising a polypeptide of the invention and a labeled substrate or ligand of such polypeptide is incubated in the absence or the presence of a candidate molecule that may be an agonist or antagonist of a polypeptide of the invention. The ability of the candidate molecule to agonize or antagonize a polypeptide of the invention is reflected in decreased binding of the labeled ligand or decreased production of product from such substrate. Molecules that bind gratuitously, i.e., without inducing the effects of a polypeptide of the invention are most likely to be good antagonists. Molecules that bind well and increase the rate of product production from substrate are agonists. Detection of the rate or level of production of product from substrate may be enhanced by using a reporter system. Reporter systems that may be useful in this regard include but are not limited to colorimetric labeled substrate converted into product, a reporter gene that is responsive to changes in polynucleotide or polypeptide activity, and binding assays known in the art.

Another example of an assay for antagonists of a polypeptide of the invention is a competitive assay that combines such polypeptide and a potential antagonist with polypeptide-binding molecules, recombinant polypeptide-binding molecules, natural substrates or ligands, or substrate or ligand mimetics, under appropriate conditions for a competitive inhibition assay. Polypeptides of the invention can be labeled, such as by radioactivity or a colorimetric compound, such that the number of such polypeptide molecules bound to a binding molecule or converted to product can be determined accurately to assess the effectiveness of the potential antagonist.

Potential antagonists include small organic molecules, peptides, polypeptides and antibodies that bind to a polynucleotide or polypeptide of the invention and thereby inhibit or extinguish its activity. Potential antagonists also may be small organic molecules, a peptide, a polypeptide such as a closely related protein or antibody that binds the same sites on a binding molecule, without inducing an activities of a polypeptide of the invention, thereby preventing the action of such polypeptide by excluding it from binding.

5 Potential antagonists include a small molecule that binds to and occupies the binding site of the polypeptide thereby preventing binding to cellular binding molecules, such that normal biological activity is prevented. Examples of small molecules include but are not limited
10 to small organic molecules, peptides or peptide-like molecules. Other potential antagonists include antisense molecules (see Okano, *J. Neurochem.* 56: 560 (1991); *OLIGODEOXYNUCLEOTIDES AS ANTISENSE INHIBITORS OF GENE EXPRESSION*, CRC Press, Boca Raton, FL (1988), for a description of these molecules). Preferred potential antagonists include compounds related to and variants of the polypeptides of the invention.

15 Each of the DNA sequences provided herein may be used in the discovery and development of antibacterial compounds. The encoded protein, upon expression, can be used as a target for the screening of antibacterial drugs. Additionally, the DNA sequences encoding the amino terminal regions of the encoded protein or Shine-Delgarno or other translation facilitating sequences of the respective mRNA can be used to construct antisense
20 sequences to control the expression of the coding sequence of interest.

The invention also provides the use of the polypeptide, polynucleotide or inhibitor of the invention to interfere with the initial physical interaction between a pathogen and mammalian host responsible for sequelae of infection. In particular the molecules of the invention may be used: in the prevention of adhesion of bacteria, in particular gram positive
25 bacteria, to mammalian extracellular matrix proteins on in-dwelling devices or to extracellular matrix proteins in wounds; to block protein-mediated mammalian cell invasion by, for example, initiating phosphorylation of mammalian tyrosine kinases (Rosenshine *et al.*, *Infect. Immun.* 60:2211 (1992); to block bacterial adhesion between mammalian extracellular matrix proteins and bacterial proteins that mediate tissue damage and; to block
30 the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques.

The antagonists and agonists of the invention may be employed, for instance, to inhibit and treat otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural

empyema and endocarditis, and most particularly meningitis, such as for example infection of cerebrospinal fluid.

Another aspect of the invention is a pharmaceutical composition comprising the above polypeptide, polynucleotide or inhibitor of the invention and a pharmaceutically acceptable carrier.

In a particular aspect the invention provides the use of an inhibitor of the invention as an antibacterial agent.

The invention further relates to the manufacture of a medicament for such uses.

The polypeptide may be used as an antigen for vaccination of a host to produce specific antibodies which have anti-bacterial action. This invention also contemplates the use of the DNA encoding the antigen as a component in a DNA vaccine as discussed more fully below.

The polypeptides or cells expressing them can be used as an immunogen to produce antibodies thereto. These antibodies can be, for example, polyclonal or monoclonal antibodies. The term antibodies also includes chimeric, single chain, and humanized antibodies, as well as Fab fragments, or the product of an Fab expression library. Various procedures known in the art may be used for the production of such antibodies and fragments.

Antibodies generated against the polypeptides of the present invention can be obtained by direct injection of the polypeptides into an animal or by administering the polypeptides to an animal, preferably a nonhuman. The antibody so obtained will then bind the polypeptides itself. In this manner, even a sequence encoding only a fragment of the polypeptides can be used to generate antibodies binding the whole native polypeptides. Such antibodies can then be used to isolate the polypeptide from tissue expressing that polypeptide.

Polypeptide derivatives include antigenically or immunologically equivalent derivatives which form a particular aspect of this invention.

The term 'antigenically equivalent derivative' as used herein encompasses a polypeptide or its equivalent which will be specifically recognised by certain antibodies which, when raised to the protein or polypeptide according to the present invention, interfere with the interaction between pathogen and mammalian host.

The term 'immunologically equivalent derivative' as used herein encompasses a peptide or its equivalent which when used in a suitable formulation to raise antibodies in a

vertebrate, the antibodies act to interfere with the interaction between pathogen and mammalian host.

In particular derivatives which are slightly longer or slightly shorter than the native protein or polypeptide fragment of the present invention may be used. In addition,

- 5 polypeptides in which one or more of the amino acid residues are modified may be used. Such peptides may, for example, be prepared by substitution, addition, or rearrangement of amino acids or by chemical modification thereof. All such substitutions and modifications are generally well known to those skilled in the art of peptide chemistry.

The polypeptide, such as an antigenically or immunologically equivalent derivative

- 10 or a fusion protein thereof is used as an antigen to immunize a mouse or other animal such as a rat or chicken. The fusion protein may provide stability to the polypeptide. The antigen may be associated, for example by conjugation, with an immunogenic carrier protein for example bovine serum albumin (BSA) or keyhole limpet haemocyanin (KLH). Alternatively a multiple antigenic peptide comprising multiple copies of the protein or 15 polypeptide, or an antigenically or immunologically equivalent polypeptide thereof may be sufficiently antigenic to improve immunogenicity so as to obviate the use of a carrier.

For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique (Kohler and Milstein, *Nature*, 256:495-497(1975)), the trioma technique, the 20 human B-cell hybridoma technique (Kozbor et al., *Immunology Today* 4:72(1983)), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole, et al., 1985, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96).

- Techniques described for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce single chain antibodies to immunogenic polypeptide 25 products of this invention.

Using the procedure of Kohler and Milstein (*supra*, (1975)), antibody-containing cells from the immunised mammal are fused with myeloma cells to create hybridoma cells secreting monoclonal antibodies.

- The hybridomas are screened to select a cell line with high binding affinity and 30 favorable cross reaction with other Streptococcal species using one or more of the original polypeptide and/or the fusion protein. The selected cell line is cultured to obtain the desired Mab.

Hybridoma cell lines secreting the monoclonal antibody are another aspect of this invention.

Alternatively phage display technology could be utilised to select antibody genes with binding activities towards the polypeptide either from repertoires of PCR amplified v-genes of lymphocytes from humans screened for possessing anti-Fbp or from naive libraries (McCafferty, J. et al., Nature 348:552-554(1990), and Marks, J. et al., Biotechnology

- 5 10:779-783(1992)). The affinity of these antibodies can also be improved by chain shuffling (Clackson, T. et al., Nature 352:624-628(1991)).

The antibody should be screened again for high affinity to the polypeptide and/or fusion protein.

As mentioned above, a fragment of the final antibody may be prepared.

- 10 The antibody may be either intact antibody of M_r approx 150,000 or a derivative of it, for example a Fab fragment or a Fv fragment as described in Skerra, A and Pluckthun, A., Science 240:1038-1040 (1988). If two antigen binding domains are present each domain may be directed against a different epitope - termed 'bispecific' antibodies.

- 15 The antibody of the invention may be prepared by conventional means for example by established monoclonal antibody technology (Kohler, G. and Milstein, C. (supra, (1975) or using recombinant means e.g. combinatorial libraries, for example as described in Huse, W.D. et al., Science 246:1275-1281 (1989).

- 20 Preferably the antibody is prepared by expression of a DNA polymer encoding said antibody in an appropriate expression system such as described above for the expression of polypeptides of the invention. The choice of vector for the expression system will be determined in part by the host, which may be a prokaryotic cell, such as *E. coli* (preferably strain B) or *Streptomyces sp.* or a eukaryotic cell, such as a mouse C127, mouse myeloma, human HeLa, Chinese hamster ovary, filarentous or unicellular fungi or insect cell. The host may also be a transgenic animal or a transgenic plant (for example, as described in 25 Hiatt, A. et al., Nature 340:76-78(1989). Suitable vectors include plasmids, bacteriophages, cosmids and recombinant viruses, derived from, for example, baculoviruses and vaccinia.

The Fab fragment may also be prepared from its parent monoclonal antibody by enzyme treatment, for example using papain to cleave the Fab portion from the Fc portion.

- 30 Preferably the antibody or derivative thereof is modified to make it less immunogenic in the patient. For example, if the patient is human the antibody may most preferably be 'humanised'; where the complimentarity determining region(s) of the hybridoma-derived antibody has been transplanted into a human monoclonal antibody , for example as described in Jones, P. et al., Nature 321:522-525 (1986), or Tempest et al., Biotechnology 9:266-273 (1991).

The modification need not be restricted to one of 'humanisation'; other primate sequences (for example Newman, R. et al., Biotechnology 10:1455-1460 (1992)) may also be used.

5 The humanised monoclonal antibody, or its fragment having binding activity, form a particular aspect of this invention.

This invention provides a method of screening drugs to identify those which interfere with the proteins selected as targets herein, which method comprises measuring the interference of the activity of the protein by a test drug. For example if the protein selected has a catalytic activity, after suitable purification and formulation the activity of the enzyme 10 can be followed by its ability to convert its natural substrates. By incorporating different chemically synthesised test compounds or natural products into such an assay of enzymatic activity one is able to detect those additives which compete with the natural substrate or otherwise inhibit enzymatic activity.

The invention also relates to inhibitors identified thereby.

15 The use of a polynucleotide of the invention in genetic immunisation will preferably employ a suitable delivery method such as direct injection of plasmid DNA into muscles (Wolff et al., Hum. Mol. Genet. 1:363 (1992); Manthorpe et al., Hum. Gene Ther. 4:419 (1993)), delivery of DNA complexed with specific protein carriers (Wu et al., J. Biol. Chem. 264:16985 (1989)), coprecipitation of DNA with calcium phosphate 20 (Benvenisty & Reshef, Proc. Nat'l Acad. Sci. USA, 83:9551 (1986)), encapsulation of DNA in various forms of liposomes (Kaneda et al., Science 243:375 (1989)), particle bombardment (Tang et al., Nature 356:152 (1992)); Eisenbraun et al., DNA Cell Biol. 12:791 (1993)) and *in vivo* infection using cloned retroviral vectors (Seeger et al., Proc. Nat'l. Acad. Sci. USA 81:5849 (1984)). Suitable promoters for muscle transfection include 25 CMV, RSV, SRa, actin, MCK, alpha globin, adenovirus and dihydrofolate reductase.

In therapy or as a prophylactic, the active agent i.e., the polypeptide, polynucleotide or inhibitor of the invention, may be administered to a patient as an injectable composition, for example as a sterile aqueous dispersion, preferably isotonic.

30 Alternatively the composition may be formulated for topical application for example in the form of ointments, creams, lotions, eye ointments, eye drops, ear drops, mouthwash, impregnated dressings and sutures and aerosols, and may contain appropriate conventional additives, including, for example, preservatives, solvents to assist drug penetration, and emollients in ointments and creams. Such topical formulations may also contain compatible conventional carriers, for example cream or ointment bases, and ethanol

or oleyl alcohol for lotions. Such carriers may constitute from about 1% to about 98% by weight of the formulation; more usually they will constitute up to about 80% by weight of the formulation.

For administration to human patients, it is expected that the daily dosage level of
5 the active agent will be from 0.01 to 10 mg/kg, typically around 1 mg/kg. The physician in any event will determine the actual dosage which will be most suitable for an individual patient and will vary with the age, weight and response of the particular patient. The above dosages are exemplary of the average case. There can, of course, be individual instances where higher or lower dosage ranges are merited, and such are within the scope of this
10 invention.

A vaccine composition is conveniently in injectable form. Conventional adjuvants may be employed to enhance the immune response.

A suitable unit dose for vaccination is 0.5-5 µg/kg of antigen, and such dose is preferably administered 1-3 times and with an interval of 1-3 weeks.

15 Within the indicated dosage range, no adverse toxicological effects are expected with the compounds of the invention which would preclude their administration to suitable patients.

In order to facilitate understanding of the following example certain frequently occurring methods and/or terms will be described.

20 "Plasmids" are designated by a lower case p preceded and/or followed by capital letters and/or numbers. The starting plasmids herein are either commercially available, publicly available on an unrestricted basis, or can be constructed from available plasmids in accord with published procedures. In addition, equivalent plasmids to those described are known in the art and will be apparent to the ordinarily skilled artisan.

25 "Digestion" of DNA refers to catalytic cleavage of the DNA with a restriction enzyme that acts only at certain sequences in the DNA. The various restriction enzymes used herein are commercially available and their reaction conditions, cofactors and other requirements were used as would be known to the ordinarily skilled artisan. For analytical purposes, typically 1 µg of plasmid or DNA fragment is used with about 2 units of enzyme
30 in about 20 µl of buffer solution. For the purpose of isolating DNA fragments for plasmid construction, typically 5 to 50 µg of DNA are digested with 20 to 250 units of enzyme in a larger volume. Appropriate buffers and substrate amounts for particular restriction enzymes are specified by the manufacturer. Incubation times of about 1 hour at 37° C are ordinarily

used, but may vary in accordance with the supplier's instructions. After digestion the reaction is electrophoresed directly on a polyacrylamide gel to isolate the desired fragment.

Size separation of the cleaved fragments is performed using 8 percent polyacrylamide gel described by Goeddel, D. *et al.*, (1980) Nucleic Acids Res., 8:4057.

5 "Oligonucleotides" refers to either a single stranded polydeoxynucleotide or two complementary polydeoxynucleotide strands which may be chemically synthesized. Such synthetic oligonucleotides have no 5' phosphate and thus will not ligate to another oligonucleotide without adding a phosphate with an ATP in the presence of a kinase. A synthetic oligonucleotide will ligate to a fragment that has not been dephosphorylated.

10 "Ligation" refers to the process of forming phosphodiester bonds between two double stranded nucleic acid fragments (Maniatis, T., *et al.*, *supra*, p. 146). Unless otherwise provided, ligation may be accomplished using known buffers and conditions with 10 units to T4 DNA ligase ("ligase") per 0.5 µg of approximately equimolar amounts of the DNA fragments to be ligated.

15 **Example 1**

Isolation of DNA coding for a virulence gene in *Streptococcus pneumoniae*

As mentioned above each of the DNAs disclosed herein by virtue of the fact that it includes an intact open reading frame is useful to a greater or lesser extent as a screen for identifying antimicrobial compounds. A useful approach for selecting the preferred DNA sequences for screen development is evaluation by insertion-duplication mutagenesis. This system disclosed by Morrison *et al.*, *J. Bacteriol.* 159:870 (1984), is applied as follows.

Briefly, random fragments of *Streptococcus pneumoniae*, strain 0100993 DNA are generated enzymatically (by restriction endonuclease digestion) or physically (by sonication based shearing) followed by gel fractionation and end repair employing T4 DNA polymerase. It is preferred that the DNA fragments so produced are in the range of 200-400 base pairs, a size sufficient to ensure homologous recombination and to insure a representative library in *E. coli*. The fragments are then inserted into appropriately tagged plasmids as described in Hensel *et al.*, *Science* 269: 400-403(1995). Although a number of plasmids can be used for this purpose, a particularly useful plasmid is pJDC9 described by Pearce *et al.*, *Mol. Microbiol.* 9:1037 (1993) which carries the erm gene facilitating erythromycin selection in either *E. coli* or *S. pneumoniae* previously modified by incorporation of DNA sequence tags into one of the polylinker cloning sites. The tagged plasmids are introduced into the appropriate *S. pneumoniae* strain selected, *inter alia*, on the basis of serotype and virulence in a murine model of pneumococcal pneumonia.

- It is appreciated that a seventeen amino acid competence factor exists (Havastein et al., *Proc. Nat'l. Acad. Sci. USA* 92:11140-44 (1995)) and may be usefully employed in this protocol to increase the transformation frequencies. A proportion of transformants are analysed to verify homologous integration and as a check on stability. Unwanted levels of reversion are minimized because the duplicated regions will be short (200-400 bp), however if significant reversion rates are encountered they may be modulated by maintaining antibiotic selection during the growth of the transformants in culture and/or during growth in the animal.
- The *S. pneumoniae* transformants are pooled for inoculation into mice, eg., Swiss and/or C57B1/6. Preliminary experiments are conducted to establish the optimum complexity of the pools and level of inoculum. A particularly useful model has been described by Veber et al. (*J. Antimicrob. Chemother.* 32:432 (1993)) in which 10^5 cfu inocula sizes are introduced by mouth to the trachea. Strain differences are observed with respect to onset of disease e.g., 3-4 days for Swiss mice and 8-10 days for C57B1/6.
- Infection yields in the lungs approach 10^8 cfu/lung. IP administration is also possible when genes mediating blood stream infection are evaluated. Following optimization of parameters of the infection model, the mutant bank normally comprising several thousand strains is subjected to the virulence test. Mutants with attenuated virulence are identified by hybridization analysis using the labelled tags from the "input" and "recovered" pools as probes as described in Hensel et al., *Science* 269: 400-403(1995). *S. pneumoniae* DNA is colony blotted or dot blotted, DNA flanking the integrated plasmid is cloned by plasmid rescue in *E. coli* (Morrison et al., *J. Bacteriol.* 159:870 (1984)) and sequenced. Following sequencing, the DNA is compared to the nucleotide sequences given herein and the appropriate ORF is identified and function confirmed for example by knock-out studies.
- Expression vectors providing the selected protein are prepared and the protein is configured in an appropriate screen for the identification of anti-microbial agents. Alternatively, genomic DNA libraries are probed with restriction fragments flanking the integrated plasmid to isolate full-length cloned virulence genes whose function can be confirmed by "knock-out" studies or other methods, which are then expressed and incorporated into a screen as described above.

The individual full length sequences given herein are summarized in the following Tables (Table 1 and Table 2). Under the column in Table 1 labeled "Identity" there is the deduced identity of each open reading frame of the invention determined using Blastp and/or MPSearch. The ORF# column indicates whether the polynucleotide encoding each

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ORF encodes more than one ORF. For example, SEQ ID NO:224 has an ORF# 1 but no #2; thus the polynucleotide encodes this ORF#1, but no other ORF was detected. On the other hand, SEQ ID NO:225 and 226 have ORF#s 1 and 2 respectively, indicating that they were both encoded by the same polynucleotide. This can also be seen in Table 2 where the 5 polynucleotide of SEQ ID NO: 2 encodes the ORFs of SEQ ID NOS: 225 and 226. Table 1 also shows the start ("START" column) and stop ("STOP" column) codons for each ORF and their positions in the encoding polynucleotide sequence. The SEQ ID NOS of the polypeptides of this table are linked to both a deduced identity in this table and a polynucleotide sequence in Table 2 which encodes each polypeptide. The "Direction" 10 column in Table 1 shows the direction of the ORF encoding each polypeptide in this table. "Forward" denotes the sense orientation and "Reverse" denotes the antisense orientation of the ORF.

TABLE 1

SEQ ID NO:	Identity	ORF #	Codon	Position			
			Start	Stop	Start	Stop	Direction
224.	Phosphate Transport ATP-Binding Protein PSTB. - Escherichia	1	-CAT	TCA-	2	553	Reverse
225.	probable ATP binding protein - Bacillus subtilis	1	-CAT	TCA-	38	781	Reverse
226.	Nopaline Transport System Permease Protein Nocm. - Agrobacterium Tumefaciens	2	-CAG	TTA-	781	1512	Reverse
227.	Aspartate Aminotransferase A (EC 2.6.11) (Transaminase A) (ASPAT.) - Rhizobium Meliloti.	1	ATG	TAG	480	671	Forward
228.	ISL2 protein - Lactobacillus helveticus	1	ATG	TAA	549	947	Forward
229.	ISL2 protein - Lactobacillus helveticus	2	ATG	TAG	889	1353	Forward
230.	Unknown	3	ATG	TGA	1421	1570	Forward
231.	Unknown	2	-CAT	CTA-	111	413	Reverse
232.	Unknown	1	ATG	TGA	133	282	Forward
233.	Acyl Carrier Protein (ACP.) - Rhizobium Meliloti.	1	-CAT	CTA-	673	906	Reverse
234.	Unknown	1	-CAT	TTA-	15	137	Reverse
235.	Unknown	2	-CAT	CTA-	681	989	Reverse
236.	Sulfate Transport System Permease Protein CYST (Fragment). - Synechocystis SP. (Strain PCC 6803).	2	-CAT	TTA-	336	689	Reverse
237.	probable transposase (insertion sequence IS861) - Streptococcus agalactiae (str a in COH-1)	2	-CAT	TCA-	149	454	Reverse
238.	Unknown	2	-CAG	TTA-	567	851	Reverse
239.	"PTS SYSTEM	1	ATG	TAA	49	477	Forward
240.	"PTS SYSTEM	2	-CAT	TTA-	151	789	Reverse
241.	nitrogen fixation protein (nifS) homolog - Haemophilus influenzae (strain Rd KW 20)	1	-CAT	TCA-	1	207	Reverse
242.	cellobiose phosphotransferase system celA - Bacillus stearothermophilus	1	-CAT	TCA-	84	431	Reverse
243.	surface protein PspA - Streptococcus pneumoniae	1	ATG	TAA	22	321	Forward
244.	Unknown	2	ATG	TAA	272	469	Forward
245.	ATP-dependent Clp proteinase (EC 3.4.21.-) chain clpL - Lactococcus lactis subs p. lactis	1	ATG	TGA	83	760	Forward

	plasmid pUCL22						
246.	Beta-Glucosidase (EC3.2.1.21) (Gentiobiase) (Cellobiase)) (Beta-D-Glucoside GL Ucohydrolyase) (Amygdalase). - <i>Bacillus Subtilis</i> .	1	-CAT	TCA-	153	599	Reverse
247.	Glycine Betaine/L-Proline Transport ATP - Binding Protein Prov. - <i>Escherichia Col. I.</i>	2	ATG	TAA	159	887	Forward
248.	Unknown	3	-CAT	TTA-	1102	1254	Reverse
249.	30S Ribosomal Protein S11 (BS11). - <i>Bacillus Subtilis</i> .	1	ATG	TGA	15	164	Forward
250.	DNA - Directed RNA Polymerase Alpha Chain (EC 2.7.7.6) (Transcriptase Alpha Chain). - <i>Bacillus Subtilis</i> .	2	ATG	TAA	282	1217	Forward
251.	Peptide Chain Release Factor 3 (RF-3). - <i>Bacteroides Nodosus</i> (<i>Dichelobacter Nod Osus</i>).	1	ATG	TAG	212	667	Forward
252.	Unknown	1	ATG	TAG	267	353	Forward
253.	Riboflavin Synthase Alpha Chain (EC 2.5.1.9). - <i>Bacillus Subtilis</i> .	2	-CAT	CTA-	213	662	Reverse
254.	Unknown	3	-CAT	TTA-	833	1045	Reverse
255.	Unknown	1	-CAT	TTA-	83	424	Reverse
256.	mesI protein - <i>Leuconostoc mesenteroides</i>	2	ATG	TAG	448	1302	Forward
257.	Transacetylase BMTD (EC 2.3.1.-). - <i>Bacillus Subtilis</i> .	1	CTG	TAG	3	320	Forward

SEQ ID NO:	Identity	ORF #	Codon	Position	Start	Stop	Direction
258.	ribose-phosphate pyrophosphokinase (EC 2.7.6.1.) - <i>Bacillus caldolyticus</i>	1	CTG	TAG	1	642	Forward
259.	Unknown	1	ATG	TAA	66	614	Forward
260.	Unknown	1	ATG	TAG	108	590	Forward
261.	nitrogenase C (nifC) homolog - <i>Haemophilus influenzae</i> (strain Rd KW20)	2	ATG	TAG	631	855	Forward
262.	Unknown	2	ATG	TAA	606	752	Forward
263.	Unknown	2	ATG	TGA	280	495	Forward
264.	Unknown	2	ATG	TGA	639	1466	Forward
265.	Acetyl Esterase (EC 3.1.---) - <i>Caldocellum Saccharolyticum</i> .	2	ATG	TAA	274	594	Forward
266.	Unknown	1	-CAT	TCA-	2	157	Reverse
267.	Triosephosphate Isomerase (EC 5.3.1.1) (TIM) - <i>Bacillus Subtilis</i> .	1	-CAT	TTA-	270	665	Reverse
268.	Branched-chain Amino Acid Aminotransferase (EC 2.6.1.42) (Transaminase B) - <i>Escherichia Coli</i> .	1	ATG	TAG	110	736	Forward
269.	branched-chain-amino-acid transaminase homolog - <i>Haemophilus influenzae</i> (strain Rd KW20)	2	ATG	TAA	708	842	Forward
270.	DnaK protein - <i>Lactococcus lactis</i>	1	CTG	TGA	3	749	Forward
271.	Ketol-Acid Reductoisomerase (EC 1.1.1.86) (Acetohydroxy-Acid Isomeroreductase) - <i>Lactococcus Lactis</i> (Subsp. <i>Lactis</i>) (<i>Streptococcus Lactis</i>)	1	ATG	TAA	99	428	Forward
272.	Unknown	1	-CAT	CTA-	278	631	Reverse
273.	Amidophosphoribosyltransferase Precursor (EC 2.4.2.14) (Glutamine Phosphoribosyl Pyrophosphate Amidotransferase) (Atase) - <i>Bacillus Subtilis</i> .	2	-CAT	CTA-	152	775	Reverse
274.	Pyrrolidone-Carboxylate Peptidase (EC 3.4.19.3) (5-Oxoprolyl-Peptidase) - <i>Streptococcus Pneumoniae</i> .	1	-CAT	TCA-	156	803	Reverse
275.	50S Ribosomal Protein L16. - <i>Mycoplasma Capricolum</i> .	1	ATG	TAA	33	416	Forward
276.	serine O-acetyltransferase (EC 2.3.1.30) - <i>Bacillus stearothermophilus</i>	2	-CAT	CTA-	577	1194	Reverse
277.	Unknown	1	ATG	TAG	61	648	Forward

278.	Unknown	1	-CAT	CTA-	165	335	Reverse
279.	Lipoprotein Signal Peptidase (EC 3.4.23.36) (Prolipoprotein Signal Peptidase) (Signal Peptidase II) (Spase II). - <i>Staphylococcus Aureus</i> .	1	ATG	TAA	56	517	Forward
280.	Unknown	1	ATG	TAA	214	534	Forward
281.	Alpha-Acetylactate Decarboxylase (EC 4.1.1.5). - <i>Bacillus Subtilis</i> .	1	-CAT	CTA-	104	445	Reverse
282.	Dihydrodipicolinate Synthase 9 (EC 4.2.1.52) (DHDPS). - <i>Bacillus Subtilis</i> .	3	-CAT	TCA-	675	884	Reverse
283.	Polyribonucleotide Nucleotidyltransferase (EC 2.7.7.8) (Polynucleotide Phosphor Ylase) (Pnpase). - <i>Photobacterium Luminescens</i> .	1	-CAT	TCA-	1	855	Reverse
284.	Single-Strand Binding Protein (SSB) (Helix-Destabilizing Protein). - <i>Bacillus S Ubtillis</i>	1	-CAT	TTA-	128	598	Reverse
285.	ATP-Dependent CLP Protease ATO-Binding Subunit CLPX. - <i>Escherichia Coli</i> .	2	-CAT	CTA-	195	482	Reverse
286.	ATP-Dependent CLP Protease ATO-Binding Subunit CLPX. - <i>Escherichia Coli</i>	4	-CAG	TCA-	676	990	Reverse
287.	N-(5'-Phosphoribosyl) Anthranilate Isomerase (EC 5.3.1.24) (PRAI). - <i>Lactococcus Lactis</i> (Subsp. <i>Lactis</i>) (<i>Streptococcus Lactis</i>).	1	ATG	TAA	83	712	Forward
288.	30S Ribosomal Protein S2. - <i>Escherichia Coli</i> .	1	ATG	TGA	277	591	Forward
289.	30S Ribosomal Protein S2. - <i>Escherichia Coli</i> .	3	ATG	TGA	918	1064	Forward
290.	Possible beta-galactosidase precursor	1	-CAT	CTA-	120	545	Reverse
291.	Unknown	1	-CAT	TTA-	77	283	Reverse
292.	Unknown	1	-CAT	TTA-	1	198	Reverse
293.	"Phospho-2-Dehydro-3-Deoxyheptonate Aldolase	1	-CAT	TTA-	217	690	Reverse

SEQ ID NO:	Identity	ORF #	Codon	Position			
			Start	Stop	Start	Stop	Direction
294.	Unknown	2	-CAT	TTA-	429	599	Reverse
295.	Unknown	3	-CAT	TCA-	739	936	Reverse
296.	Sorbitol Dehydrogenase (EC 1.1.1.14) (L-Iditol 2-Dehydrogenase). - <i>Bacillus Subtilis</i> .	1	ATG	TAA	64	480	Forward
297.	EBG Operon Repressor. - <i>Escherichia Coli</i> .	2	-CAT	CTA-	668	1060	Reverse
298.	cellobiose phosphotransferase system celA - <i>Bacillus stearothermophilus</i>	2	-CAT	TTA-	249	566	Reverse
299.	Unknown	3	-CAT	TCA-	581	964	Reverse
300.	Adenylosuccinate Lyase (EC 4.3.2.2) (Adenylosuccinase) (ASL). - <i>Bacillus Subtilis</i> .	1	-CAT	TTA-	99	809	Reverse
301.	ATP-Binding Protein BEXA. - <i>Haemophilus Influenzae</i> .	1	ATG	TGA	111	404	Forward
302.	L-Lactate Dehydrogenase (Cytochrome) (EC 1.1.2.3). - <i>Escherichia Coli</i> .	2	ATG	TAA	337	507	Forward
303.	Phosphate Transport System Permease Protein PSTC. - <i>Escherichia Coli</i> .	3	ATG	TGA	507	1070	Forward
304.	Sulfate Transport ATP-Binding Protein CysA. - <i>Synechococcus SP. (Strain PCC 7942) (Anacystis Nidulans R2)</i> .	1	-CAT	CTA-	110	838	Reverse
305.	Unknown	2	-CAT	TTA-	838	1077	Reverse
306.	Unknown	2	-CAT	TCA-	282	749	Reverse
307.	Unknown	2	ATG	TAG	1108	1290	Forward
308.	Phosphoribosylformylglycinamide Cyclo-Ligase (EC 6.3.3.1) (AIRS) (Phosphoribosyl-Aminoimidazole Synthetase) (AIR Synthase). - <i>Bacillus Subtilis</i> .	2	-CAT	TCA-	331	477	Reverse
309.	Unknown	2	ATG	TAA	313	765	Forward
310.	SMS Protein. - <i>Escherichia Coli</i> .	1	-CAT	TCA-	102	416	Reverse
311.	sigma 42 protein - <i>Enterococcus faecalis</i>	1	-CAT	TCA-	8	487	Reverse
312.	Unknown	1	-CAT	TTA-	76	390	Reverse
313.	Guanylate Kinase (EC 2.7.4.8) (GMP Kinase). - <i>Escherichia Coli</i> .	2	-CAG	TTA-	415	849	Reverse
314.	Unknown	1	-CAT	TCA-	51	296	Reverse
315.	Unknown	1	ATG	TAA	175	285	Forward
316.	Unknown	2	ATG	TAA	361	558	Forward
317.	Unknown	3	ATG	TAA	383	1144	Forward

318.	"PTS System	2	-CAT	TCA-	166	465	Reverse
319.	L-Fucose Isomerase (EC 5.3.1.-) - Escherichia Coli.	1	-CAT	CTA-	9	482	Reverse
320.	Unknown	2	-CAT	TTA-	495	650	Reverse
321.	Unknown	1	ATG	TGA	130	231	Forward
322.	3-Oxoacyl-[Acyl-Carrier Protein] Reductase (EC 1.1.1.100) (3-Ketoacyl- Acyl Carrier Protein Reductase). - Escherichia Coli.	1	-CAT	TCA-	51	200	Reverse
323.	3-Oxoacyl-[Acyl-Carrier Protein] Reductase (EC 1.1.1.100) (3-Ketoacyl- Acyl Carrier Protein Reductase). - Escherichia Coli.	2	-CAT	TCA-	231	614	Reverse
324.	2-Isopropylmalate Synthase (EC 4.1.3.12) (Alpha-Isopropylmalate Synthase) (Alpha A-IPM Synthetase). - Lactococcus Lactis (Subsp. Lactis) (Streptococcus Lactis).	1	-CAT	TTA-	31	231	Reverse
325.	2-Isopropylmalate Synthase (EC 4.1.3.12) (Alpha-Isopropylmalate Synthase) (Alpha A-IPM Synthetase). - Lactococcus Lactis (Subsp. Lactis) (Streptococcus Lactis).	2	-CAT	TCA-	191	334	Reverse
326.	Unknown	3	-CAT	TCA-	309	452	Reverse
327.	2-Isopropylmalate Synthase (EC 4.1.3.12) (Alpha-Isopropylmalate Synthase) (Alpha A-IPM Synthetase). - Lactococcus Lactis (Subsp. Lactis) (Streptococcus Lactis).	4	-CAT	TTA-	495	1127	Reverse
328.	Unknown	2	-CAT	TCA-	170	469	Reverse
329.	Unknown	1	ATG	TAG	105	473	Forward
330.	Strscaa Ncbi gi: 310629NCBI gi: 473 - Streptococcus gordonii (strain PK488) DNA	1	-CAG	CTA-	81	665	Reverse

SEQ ID NO:	Identity	Codon		Position		Direction
		ORF #	Start Stop	Start	Stop	
331.	Unknown	1	ATG	TGA	228	374 Forward
332.	Lysyl Aminopeptidase (EC 3.4.11.15) precursor - <i>Lactococcus lactis</i>	1	-CAT	TCA-	107	766 Reverse
333.	Indole-3-Glycerol Phosphate Synthase (EC 4.1.1.48) (IGPS). - <i>Lactococcus Lactis</i> (SUBSP. <i>Lactis</i>) (<i>Streptococcus Lactis</i>)	1	-CAT	TCA-	127	369 Reverse
334.	Anthraniate Phosphoribosyltransferase (EC 2.4.2.18). - <i>Lactococcus Lactis</i> (Sub SP. <i>Lactis</i>) (<i>Streptococcus Lactis</i>)	2	-CAA	TCA-	366	641 Reverse
335.	Tagatose-6-Phosphate Kinase (EC 2.7.1.-) (Phosphotagatokinase). - <i>Lactococcus L Actis</i> (Subsp. <i>Lactis</i>) (<i>Streptococcus Lactis</i>)	1	ATG	TGA	42	524 Forward
336.	Unknown	1	ATG	TGA	73	474 Forward
337.	Unknown	1	-CAT	TTA-	32	286 Reverse
338.	Unknown	1	ATG	TGA	306	572 Forward
339.	Acetolactate Synthase Large Subunit (EC 4.1.3.18) (AHAS) (Acetylhydroxy-Acid Syn thase Large Subunit) (ALS). - <i>Lactococcus Lactis</i> (SUBSP. <i>Lactis</i>) (<i>Streptococcus Lactis</i>).	1	ATG	TAG	59	502 Forward
340.	Penicillin-Binding Proteins 1A/1B. - <i>Bacillus Subtilis</i> .	2	ATG	TGA	535	720 Forward
341.	Unknown	1	ATG	TAG	165	488 Forward
342.	Anthraniate Phosphoribosyltransferase (EC 2.4.2.18). - <i>Lactococcus Lactis</i> (SUB SP. <i>Lactis</i>) (<i>Streptococcus Lactis</i>).	1	-CAT	TCA-	5	394 Reverse
343.	grpE protein - <i>Lactococcus Lactis</i>	2	ATG	TAA	124	543 Forward
344.	Unknown	1	-CAT	CTA-	34	195 Reverse
345.	Unknown	2	-CAT	TTA-	377	544 Reverse
346.	Unknown	2	ATG	TAA	159	503 Forward
347.	Unknown	2	-CAT	CTA-	315	644 Reverse
348.	Unknown	2	-CAT	CTA-	468	587 Reverse
349.	Unknown	2	-CAT	CTA-	482	631 Reverse
350.	Unknown	2	-CAT	TTA-	380	757 Reverse
351.	NIFS Protein Homolog (Fragment). - <i>Lactobacillus Delbrueckii</i> (SUBSP. <i>Bulgaricus</i>).	1	ATG	TAG	87	797 Forward
352.	"Ornithine Carbamoyltransferase	1	TTG	TAA	2	502 Forward

353.	PSEG LI NCB1 gi: 499660 - Pseudomonase putida.	1	-CAT	TTA~	50	481	Reverse
354.	Unknown	1	CTG	TAA	1	522	Forward
355.	Thioredoxin. - Streptomyces Clavuligerus.	1	ATG	TAG	58	375	Forward
356.	D-alanine permease (dagA) homolog - Haemophilus influenzae (strain Rd KW20)	1	ATG	TAG	185	343	Forward
357.	Unknown	1	-CAT	TTA~	78	371	Reverse
358.	"DNA Polymerase III	1	-CAA	TCA~	82	561	Reverse
359.	Transport ATP-Binding Protein Coma. - Streptococcus Pneumoniae.	1	-CAT	TTA~	112	552	Reverse
360.	Unknown	2	ATG	TAA	445	540	Forward
361.	surface protein PspA - Streptococcus pneumoniae	1	-CAT	TCA~	45	416	Reverse
362.	Licid Protein. - Haemophilus Influenzae	2	ATG	TAA	268	633	Forward
363.	Unknown	2	ATG	TAA	527	640	Forward
364.	Glutamine Transport ATP- Binding Protein GLNQ. - Escherichia Coli.	1	CTG	TGA	1	393	Forward
365.	Unknown	1	ATG	TAG	184	303	Forward
366.	Unknown	1	ATG	TGA	794	919	Forward
367.	Lipoamide Dehydrogenase Component (E3) of Pyruvate Dehydrogenase Complex (EC 1.8.1.4) (Dihydrolipoamide Dehydrogenase). - Azotobacter Vinelandii.	1	ATG	TAA	3	416	Forward

SEQ ID NO:	Identity	ORF #	Codon	Position			
			Start	Stop	Start	Stop	Direction
368.	Orotate Phosphoribosyltransferase (EC 2.4.2.10) (OPRT). - <i>Bacillus Subtilis</i> .	1	-CAT	CTA-	21	311	Reverse
369.	Unknown	1	ATG	TAA	28	309	Forward
370.	SPOOB-Associated GTP-Binding Protein. - <i>Bacillus Subtilis</i> .	1	ATG	TGA	110	538	Forward
371.	Transport ATP-Binding Protein COMA. - <i>Streptococcus Pneumoniae</i> .	1	-CAA	TCA-	47	679	Reverse
372.	prephenate dehydrogenase (EC 1.3.1.12) - <i>Lactococcus lactis</i> .	2	ATG	TAG	271	492	Forward
373.	O-Sialoglycoprotein Endopeptidase (EC 3.4.24.57) (Glycoprotease). - <i>Pasteurella Haemolytica</i> .	1	CTG	TAA	1	450	Forward
374.	Unknown	1	-CAT	TTA-	7	282	Reverse
375.	Unknown	1	TTG	TAA	2	265	Forward
376.	"DNA Polymerase III	1	ATG	TGA	3	401	Forward
377.	Unknown	2	ATG	TAA	361	516	Forward
378.	Dihydrodipicolinate Synthase (EC 4.2.1.52) (DHDPS). - <i>Bacillus Subtilis</i> .	1	-CAT	TTA-	179	457	Reverse
379.	Unknown	2	-CAT	TCA-	104	322	Reverse
380.	Unknown	2	-CAT	TCA-	248	649	Reverse
381.	Unknown	1	-CAT	TTA-	56	394	Reverse
382.	Unknown	2	-CAT	TTA-	254	409	Reverse
383.	Unknown	1	ATG	TAG	138	617	Forward
384.	Unknown	2	-CAT	TTA-	225	479	Reverse
385.	Unknown	2	ATG	TAA	747	857	Forward
386.	Unknown	1	ATG	TAG	294	443	Forward
387.	Unknown	2	ATG	TGA	356	544	Forward
388.	Unknown	1	-CAT	CTA-	4	141	Reverse
389.	Unknown	1	CTG	TAG	1	579	Forward
390.	Unknown	2	-CAT	TTA-	309	452	Reverse
391.	Phosphopentomutase (EC 5.4.2.7). - <i>Escherichia Coli</i> .	1	ATG	TAA	3	233	Forward
392.	D-Alanyl-D-Alanine Carboxypeptidase Precursor (EC 3.4.16.4) (DD-Peptidase)(DD-Carboxypeptidase)(Cpase)(PBP5). - <i>Bacillus Subtilis</i> .	1	-CAT	TTA-	52	537	Reverse
393.	Na+ and Cl-dependent gamma-aminobutyric acid transporter homolog-Haemophilus	1	TTG	TGA	2	268	Forward

	influenzae (strain Rd KW20)						
394.	Unknown	2	ATG	TGA	319	546	Forward
395.	dihydrolipoamide dehydrogenase (EC 1.8.1.4) - <i>Pelobacter carbinolicus</i>	1	ATG	TGA	3	284	Forward
396.	Unknown	2	ATG	TGA	241	450	Forward
397.	Beta-Glucosidase A (EC 3.2.1.21)(Gentobiase)(Cellobiase)(Beta-D-Glucoside Glucohydrolase). - <i>Clostridium Thermocellum</i> .	1	ATG	TAA	184	453	Forward
398.	Uracil Permease. - <i>Bacillus Caldolyticus</i> .	1	ATG	TAA	93	353	Forward
399.	Unknown	2	ATG	TAG	127	516	Forward
400.	ligoendopeptidase F- <i>Lactococcus lactis</i>	1	ATG	TGA	134	310	Forward
401.	Stratpasea NCBI gi: 153565NCBI gi: 4- Streptococcus Faecalis DNA.	2	ATG	TAA	392	568	Forward
402.	Unknown	2	ATG	TAA	376	507	Forward
403.	Exodeoxyribonuclease Small Subunit (EC 3.1.11.6) (Exonuclease VII Small Subunit). - <i>Escherichia Coli</i> .	2	-CAT	TCA-	470	682	Reverse
404.	ATP-Dependent DNA Helicase RECG (EC 3.6.1.-). - <i>Escherichia Coli</i> .	1	ATG	TGA	3	455	Forward

SEQ ID NO:	Identity	ORF #	Codon	Position			
			Start	Stop	Start	Stop	Direction
405.	Possible thiamin biosynthetic enzyme	1	-CAT	TTA-	15	347	Reverse
406.	SPOU Protein. - Escherichia Coli.	2	ATG	TAA	322	618	Forward
407.	Malonyl Coa-Acyl Carrier Protein Transacylase (EC 2.3.1.39). - Escherichia Coli.	1	ATG	TAG	85	498	Forward
408.	Unknown	1	-CAT	CTA-	17	118	Reverse
409.	nucleoside diphosphate kinase (ndk) homolog- Haemophilus influenzae (strain Rd KW20)	1	CTG	TGA	1	159	Forward
410.	Nucleoside Diphosphate Kinase (EC 2.7.4.6)(NDK) (NDP Kinase). - Escherichia Co Li.	2	ATG	TAG	215	481	Forward
411.	Unknown	1	-CAT	TTA-	21	368	Reverse
412.	Unknown	2	-CAT	TCA-	162	314	Reverse
413.	Unknown	1	ATG	TAA	187	417	Forward
414.	Unknown	2	ATG	TGA	316	417	Forward
415.	Unknown	1	ATG	TGA	316	453	Forward
416.	Enolase (EC 4.2.1.11)(2-Phosphoglycerate Dehydratase)(2-Phospho-DOGlycerate Hydro-Lvase). - Bacillus Subtilis.	1	-CAT	TTA-	4	435	Reverse
417.	Unknown	1	CTG	TGA	1	363	Forward
418.	Unknown	1	ATG	TGA	39	383	Forward
419.	PILB Protein. - Neisseria Gonorrhoeae.	1	-CAT	TTA-	145	327	Reverse
420.	Unknown	2	ATG	TGA	285	533	Forward
421.	Unknown	1	CTG	TAG	2	379	Forward
422.	integrase/recombinase (xprB) homolog - Haemophilus influenzae (strain Rd KW20)	1	ATG	TAA	305	421	Forward
423.	Unknown	1	-CAT	CTA-	173	436	Reverse
424.	Unknown	1	-CAT	CTA-	182	427	Reverse
425.	Unknown	1	ATG	TAA	49	372	Forward
426.	"Mutator Mutt Protein (7	1	-CAT	CTA-	21	446	Reverse
427.	Unknown	1	ATG	TGA	177	380	Forward
428.	Possible phosphatase	1	ATG	TAG	112	402	Forward
429.	Unknown	1	ATG	TGA	110	271	Forward
430.	Phosphoenolpyruvate Carboxylase (EC 4.1.1.31). - Corynebacterium Glutamicum.	2	ATG	TGA	337	561	Forward
431.	Unknown	1	ATG	TGA	214	324	Forward
432.	50S Ribosomal Protein L31. - Bacillus	1	ATG	TAA	142	426	Forward

	<u>Subtilis.</u>						
433.	glycosyl transferase (IgtD) homolog - <i>Haemophilus influenzae</i> (strain Rd KW20)	1	ATG	TGA	127	399	Forward
434.	Unknown	2	-CAT	CTA-	244	435	Reverse
435.	Unknown	2	ATG	TGA	118	309	Forward
436.	Factor essential for Expression of Methicillin Resistance. - <i>Staphylococcus Aur Eus.</i>	2	-CAT	TTA-	168	434	Reverse
437.	Unknown	1	-CAT	TCA-	2	214	Reverse
438.	Unknown	1	TTG	TAA	2	142	Forward
439.	Unknown	1	ATG	TAA	30	191	Forward

SEQ ID NO:	Identity	ORF #	Codon	Position		Direction
			Start	Stop	Start	
440.	Aspartate Aminotransferase (EC 2.6.1.1) (Transaminase A)(ASPAT). - Bacillus SP. (STRAIN YM-2).	1	-CAT	TCA-	63	416 Reverse
441.	Unknown	1	ATG	TAA	52	342 Forward
442.	Unknown	2	-CAT	TCA-	210	455 Reverse
443.	Unknown	1	TTG	TGA	2	517 Forward
444.	ATP-Dependent DNA Helicase RECG (EC 3.6.1.-) - Escherichia Coli.	1	ATG	TGA	83	376 Forward
445.	Unknown	1	ATG	TAA	70	384 Forward
446.	Cell Division Protein FTSA. - Bacillus Subtilis.	1	TTG	TAA	3	371 Forward
447.	Unknown	1	ATG	TAG	70	441 Forward
448.	Unknown	1	ATG	TAG	104	454 Forward
449.	Unknown	1	CTG	TAA	1	159 Forward
450.	Unknown	1	ATG	TAA	120	347 Forward
451.	Unknown	1	ATG	TGA	31	423 Forward
452.	Unknown	2	ATG	TGA	225	416 Forward
453.	Unknown	1	ATG	TGA	290	418 Forward
454.	Unknown	1	ATG	TGA	3	269 Forward
455.	JAG Protein (SPOIIJ Associated Protein). - Bacillus Subtilis.	1	ATG	TGA	93	365 Forward
456.	"DNA -3-Methyladenine Glycosidase I (EC 3.2.2.20)(3-Methyladenine-DNA Glycosylase I	1	ATG	TAG	91	282 Forward
457.	"Glucan I	1	-CAT	TTA-	4	150 Reverse
458.	Unknown	1	-CAT	CTA-	245	400 Reverse
459.	Glutamate/Aspartate Transport ATP-Binding Protein GLTL. - Escherichia Coli.	1	-CAT	TCA-	81	218 Reverse
460.	Unknown	1	-CAT	TTA-	103	492 Reverse
461.	Unknown	1	ATG	TGA	305	484 Forward
462.	Unknown	1	-CAT	TCA-	29	355 Reverse
463.	Unknown	2	-CAT	TTA-	572	838 Reverse
464.	Unknown	2	-CAT	TCA-	652	1026 Reverse
465.	Unknown	2	-CAT	TTA-	318	764 Reverse
466.	Unknown	2	ATG	TGA	719	805 Forward
467.	Llcpqrda NCB1 gi: 511014 - Lactococcus lactis.	1	ATG	TGA	134	472 Forward

468.	Unknown	1	ATG	TGA	385	492	Forward
469.	Unknown	2	ATG	TAA	587	721	Forward
470.	galE protein - <i>Neisseria meningitidis</i>	1	-CAT	TCA-	23	460	Reverse
471.	Unknown	2	-CAG	TTA-	717	1319	Reverse
472.	Naphthoate Synthase (EC 4.1.3.36) (Dihydroxynaphthoic Acid Synthetase)(Dhna Sy Nthetase). - <i>Escherichia Coli</i> .	1	ATG	TGA	97	414	Forward

SEQ ID NO:	Identity	Codon		Position		Direction
		ORF #	Start Stop	Start	Stop	
473.	Unknown	1	CTG TGA	1	246	Forward
474.	Unknown	1	-CAT TCA-	341	748	Reverse
475.	Unknown	1	-CAT TTA-	217	858	Reverse
476.	Unknown	1	-CAT TTA-	499	729	Reverse
477.	Multiple Sugar-Binding Transport ATP-Binding Protein MSMK. - Streptococcus MUTA NS.	2	ATG TAA	407	571	Forward

Table 2 shows the correlation between the SEQ ID NO of each DNA sequence of the invention with the SEQ ID NO(S) of polypeptide or polypeptides that its open reading frame(s) encodes. For example, the DNA of SEQ ID NO:1 encodes one polypeptide, that of SEQ ID NO:224. Whereas, the DNA of SEQ ID NO:2 encodes two polypeptides, the polypeptides of SEQ ID NO:225 and SEQ ID NO:226.

TABLE 2

DNA	Protein (open reading frame)
1	224
2	225,226
3	227
4	228,229,230
5	231
6	232
7	233
8	234
9	235
10	236
11	237
12	238
13	239
14	240
15	241
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17	243,244
18	245
19	246
20	247,248
21	249,250
22	251
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24	253,254
25	255,256
26	257
27	258
28	259
29	260,261
30	262

31	263
32	264
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35	267
36	268,269
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47	280
48	281
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52	285,286
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54	288,289
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64	302,303
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76	319,320
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78	322,323
79	324,325,326,327
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85	333,334
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95	344,345
96	346
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211	462,463
212	464
213	465
214	466
215	467
216	468,469
217	470,471
218	472
219	473
220	474
221	475
222	476
223	477

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Black, Michael
Hodgson, John
Knowles, David
Nicholas, Richard
Stodola, Robert

(ii) TITLE OF THE INVENTION: Novel Compounds

(iii) NUMBER OF SEQUENCES: 477

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SmithKline Beecham Corporation
(B) STREET: 709 Swedeland Road
(C) CITY: King of Prussia
(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 19406-0939

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 01-APR-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/014690
(B) FILING DATE: 02-APR-1996

PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/025788
(B) FILING DATE: 22-AUG-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Gimmi, Edward R
(B) REGISTRATION NUMBER: 38,891

(C) REFERENCE/DOCKET NUMBER: P50466

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 610-270-4478
- (B) TELEFAX: 610-270-5090
- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 683 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCAAACATG	GTCTCTTCTA	GTTGCATGGT	CGCAATCGGA	TCCAAGGCTG	AGGCTGGGCT	60
CATCCATTAA	GAGGATATCT	GGCTTAACAG	AGATGGCACG	AGCGATACAG	AGACGTTGTT	120
GCTGACCACC	TGATAAGGTC	AAGGCTGACT	TGTGGAGATC	GTCTTAACC	TGATCCAAA	180
GGGCAGCCTG	ACTAAGGGAG	GTTTCTACGA	TTTCATCTAG	GACTTGCTTA	TCCTTAACTC	240
CAGCACGTTTC	ATGCGAAAG	GTAATATTAC	GGTAAATTGA	CTTAGCAAAT	GGATTGGGGC	300
GTTGAAAAC	CATTCCAATG	TGTTTACGCA	TTTCATAAAAC	GTTGATTTCT	GGACGGTTGA	360
CATCAATTCC	ACGATAGAGA	ATCTGCCAG	TTACTTTAGC	AATATCAATG	GTATCATTCA	420
TGGGATTGAG	ACTGCGTAAG	TAGGTAGATT	TCCCCGATCC	CGACGGACCA	ATCAAAGCTG	480
TAATTTTATT	TCCTTCAAA	TTGCATATCA	ATCCCCTTAA	TGGATTTCATT	TTTACCATAG	540
TAAACATGGA	CATCCTTAGT	AGAAAAGGCT	ACTTTTCTT	CAGGAAAGGT	AAGGATATGC	600
TTCTCATCCC	AGTTATATGT	TGACATGGCT	TCTCCTTCTAG	GCAGCGGTTA	ATTCTTGTG	660
TAGATAGCTT	CCGAACTTAC	GAG				683

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTAGTCCAAC TAACTGAGTT TTCCTTTATC TATTATATCA AATATAAGTC CGTTTGTAAC 60
 TAGTGAAGAA TTCTTTGTC CGCTCTTCTT TAGGGGTGTG GATAATCTCA TCCGGAGTTTC 120
 CAGACTCGAT GATTTTCCCC TTATCTAAGA AGAGAATTTC ATCCGCAACT TGGGCTACAA 180
 AGGGCATGTC ATGACTGACC AAAATCATGG TCTGACCTGA CTTAGCAGCA TCTGCAATAG 240
 ACTTTCTAC TTCACCGACC AATTCTGGGT CAAGGGCTGA AGTTGGTTCG TCTAAGAGCA 300
 AACACATCTGG TTTCATAGCA AGCGCACCGC CTAGGGCAAC CCGTTGCTTC TGTCCACCTG 360
 ATAAAATGGCG AGGATAATGG TTTTCACGGT CCGAAAGCCC AACCTTAGCC AACTCTTCCT 420
 TGCGAACATCTT AGTCGCTTCT TGCGCAGATA ATTCTTGAC AACAAACCAAG CCTTCTTTCA 480
 CATTATCAAG TGCTGTTCGG CGTTCAAATA AATTAAACTG TTGGAAAACC ATAGACAAC 540
 TACGGCGTAG GGCAAGGATT TCTTCTTGAG TGATTITAGA AAAATCACT GAAAAACCAT 600
 CAATCTGAAT AGAGCCACTG TCAGGTGTTT CAAGATAATT GAGACTGCGA AGAAAGGTTG 660
 ATTTTCCAGC TCCTGAAGAA CCAATCAAGG CTACAACCTTC CCCTTTTGA ATATCCAAGT 720
 TCAGATGATC CAAGACAGTC TGTCTGAAA AGGATTGCT TAAATTGAA ATCTTAATCA 780
 TTAACGAAGG TCTCCTTTCA CATCTGTTG CACTGTATCA GGTGCAGAAA TAGCCATTTC 840
 TCTCTCGATG AAACGACCGA GGCTTCAAT TCCGATATTG ACTACCCAAT AAACAAGGGC 900
 AACAGAGATG AAGCGTCAA AATAGCGATA ATCAGCTCCA CCTAGAAATCT GAGCTTGGC 960
 AAAGACTTCC ACAACACCCG CACTAAAAGC TAGAGATGTT CCCTTGGTCA AACCGATGAG 1020
 GGAATTAAATC AAGGTTGGAG TAGCTACAC CGCTGCATTA GGAATAATCA CTCGTCGATA 1080
 AACTTGCGCT CGGGTCATAC CCAGACTGCG CGCCGCCTCA ATCTCACCAG GATTAACGTGA 1140
 GAGAATGGCT GCACGAATGG TTTCACTAGC ATAAGCTGCC TCATTAAGG CAAAAGCCAC 1200
 AATCGCAAA GCTGCAGCTG GAATCGCATT GATATTGAGA CCAGTTCCCG ATTGCTGATT 1260
 GAGGGCTTTC AAAGCCAAAG GGATTCGTA GTAGGTCAAC ATGAGTTGCA CCAAAATCGG 1320
 TGTCCTTTT AAGAAACTAA CAAAGAAGGC CTGCAAGGGA TATAAAATCT TGACACGATT 1380
 GATCTTCACA ATGGCAAAA GAAGCGCCAA ACCAAGCCA AAAAGGGCAC CGCCAATTGT 1440
 CAACATAATT GTTGTGGAA GTTGTGGAC AATTCTAGGG ATTCCATCAA AGACCGAACG 1500
 TAGGCTAAAC AG 1512

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGGAGATTA TTGAGATTGC CCGTCAAAAC GATTTGATTA TNNTTGCAGA TGAAATCTAT 60
 GACGGCATGG TAAATGGACG GACATGTGCA TAACGCCCTGT GGCGAGCTTG GCACCCAGATG 120
 TCTTCTGTGT CAGCATGAAT CGCTGTCAA AATCCCACCG CATAGCAGGT TTCCCGTGTG 180
 GGATGGATGG TCTTGTCTGG CCCTAAGACT CATGTTAAGG GCTATATCGA AGGGCTCAAT 240

ATGCTGTCCA ATATGCGCCT TTGCTCTAAC GTTTTGGCTA CCAACGCTGC ATTAGGAATA	300
ATCACTGTCG TACAAACTTG CGCTTGGGGG GTCACCAATC AGTCGATGAA TTGCTTCTTC	360
CTGGTGGACG AATCTACGAG CAAAGAAATT TCATCTATAA TGCCATTCAA GATATTCCAG	420
GTTTGTCTGC CGTTAAACCC AAGGCGGGGC TCTATATCTT CCCAAAAATC GACCGCAATA	480
TGTACCGTAT CGATGATGAT GAGCAGTTG TCCCTGATTT CTTGAAGCAG GAAAAGGTTC	540
TCTTGGTCA TGGTCGAGGC TTTAACTGGC AGGAACCAGA CCACCTCCGT ATCGTTTACC	600
TTCCCTCGTGT TGATGAGTTA GCCCAAATCC AAGAAAAGAT GACTCGTTTC TTGAAACAGT	660
ATCGTAGATA GGGCTTGCAT TCGAAAAAGC TGGAAACATT TGCCTAGAG	709

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTGCTTCAGA ACCTGCCAAA CCAGCACCGA TAACATTGAT ATAAGATTGA GACACGACAC	60
TAATACCTCT TTGGGAGTGT GAAGTTAAGA TTCACATTGA AAAAGCCAAT CAGACATTACA	120
AGCTTTGAG TTTCTTGGCT CAGGCTGAAA AAGTCCACAG GGCTTTNCA CTCCCCACAAA	180
TCTTCTATT TTTTCTNCTA CTAGTATAAC AAAAAAAAGGG AAGAAGGNAAC ACTTCCCTGT	240
TTAGTCATTT TCTTGATGTA AAGAGATAGT GAGTATTCCA GTTAAGAACATC AATTATATGC	300
TACTCTATAA AATCTTTTCC ACATAACCGA TCGATAGGGA CTGTTATTCT ATCTCTTGCT	360
ATAACCGTAT TATCTAAAAC AGCATAACAT TCAACATAGT GATCTCCCTT AACTGTGAA	420
TCTTCCGTGA TATTTTATTCTT TACCTGAAAA AATAGCACAC GCTCACAAATT CTTCTTAATA	480
GCCTCAGCTT CAATATTCT TACTTTCCAA TAGACTCCCT GCGAAACAAA ATATGGTATA	540
GTAGTTCTAT GAATGATGAA GCAAGTAAAC AACTAATGTA TGCACGATTT AAGCGTCTTG	600
TTGGTGTCA GCGCACGACT TTTGAAGAGA TATTAGCTGT ATTAAAAACA GCTTATCAAC	660
TTAAACACGC AAAAGGTGGA CGAAAACCTA AATTAAGCCT AGAAGACCTT CTTATGGCCA	720
CTCTTCAATA TGTGGAGAA TATCGAACCTT ATGAACAAAT TCGGGCTGAT TTTGGTATCC	780
ACGAAAGCAA CTTAACCGT CGGAGCCAAT GGGTTGAAGT AACTCTTGT CAAAGTGGTG	840
TTACGATTTC AAGAACCTCT CTCAGTTCTG AGGACACGGT AATGATTGAT GCGACCGAAG	900
TACAAATCAA TCGCCCTAAA AAAAGAATTAA CGGAATCATT CTGGTAAAAAA GAAATTTCAC	960
GCTATGAAGG CTCAAGCGAT TGTACAAGT CAAGGGAGAA TTGTTCTTT GGATATCGCT	1020
GTGAACTATA GTCATGATAT GAAGTTGTTG AAAATGAGTT GCAGAAATAT CGGACAAAGCT	1080
GGAAAAATCT TGGCTGATAG TGTTTATCAA GGGCCCATGA AGATATATCC TCAAGCACAA	1140
ACTCCACGTA AATCCAGCAA ACTCAAGCCG CTAATAGCTG AAGATAAAAGC TTATAACCCT	1200
GCGCTATCCA AGGAGAGAAG CAAGGTTGAG AACATCTTGC CAAAGTAAA AACGTTAAA	1260
ATGTTTCAA CAACCTATCG AAATCATCGT AAACGCTTCG GATTACGAAT GAATTGATT	1320
GCTGGCATTAA TCAATTATGA ACTAGGATTG TAGTTTGCA GGAAGTCTAT TATTTCCCTT	1380

ATTGTCTGTA AGTCTACTGA CCTTGTGTT TATCCCAGTC ATGGTTCTA GTTCGGGCTC	1440
AGAGTTCAA AGTGGATGGC AAGAGCATCA ATTGATTGCT GAGAAGGTTA GTAAAACACT	1500
TGACAAGACA TTTGATAAGG ATGTCAGAAA AATTCCGACC AGTCCAGTTT TATCAAAAT	1560
TTGTAGATGA GATGGGAAGG ATTACTC	1588

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTGTTTTAA TACAGCTAAC ATCTCTCAA AAGTGGTACG CTGAACACCA ACAAGACGCT	60
TAAATCGTC ATCAGTTAGT TGTTTACTTG CTTCATCATT CATAGAACTA CTATACCATA	120
TTTGTGTTCG CAGGGAGTCT AATATTGTCA AATACTGGAG CGCTCATTGC TGGTATACGG	180
AATAAGATTG GCCCAGCTTC GATAACTGGG ATACCTGGTT CAAAACCAAG ATCTGTTGCA	240
GCGATTGGTG TAAAGATATC GTAACCTTTC ATAAGGTCTT CGTTTACATC TTTCACCATG	300
ACTGCATCAC AGTGAACATC ATAACCACGG TTTGAAAGTT CTTCTCTAG AGCACTTTA	360
ATTTGGTGAC TTGAGTTAAC ACCTGCACCG CAGGCAGCAA GAATTTAAT CATTAGATT	420
TCCTCCGATT TTATTTTTA ATAGACAAGA TTAAGCGGTT GCTTCAGCAA TGTAAGCATA	480
AAGTTTTCT GGTTCGAAA TTTTGATAG GTCTCAAGA TGTCCATTTC CTGTGAAAAA	540
GTCCCATCAAC TGAGCCAGAA TATTTGTTTG ACTTGAACCT GAGTTATTGA TGATAAAAGAA	600
GAGCAAGGAT ACTTCTACTT CCTTATCAGG AGCTATCATA TTGTGAAAAG TTACTGATTT	660
TTCTAATCGA ACAACCACCA CTTTCTCAG	690

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ACTGCTACCT TTAAGAAGAT AGTAGACGTA TATACCTTTT TAAGAAAATC AAAAAGATAC	60
TATAAAAAAT CTATTTGTTT ATGAAATTAA AGACTTTGGT AACAAATTGA AAATAAAAAG	120

GAGGTATTCA TCATGAATAC AAAAATGATG TCACAATTTC CTGTTATGGA TAATGAAATG	180
CTTGCTTGC G TTGAAGGTGG AGATATTGAT TGGGAAAGAG AAATTAGTTG TGCAGCAGGG	240
GTTGCATATG GCGCAATTGA TGCGTGTGCA ACAACGGTTT GATATTCTA TTGGGACCAT	300
TTGCTATAGG AATAGGTGTA ACTGGTGCTG CAGGTGGAG	339

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTGAAGACCT CGTGCTACTC CTCCCTCAAAC ACCTGCTTTC GCAAAATCTC CCCAATTGCA	60
TCCGCCACCT TCAACTCAAG CAAGCATCTC AGTATCCATA ATTTCAAATT GTGACATCTT	120
TTTTGTATTTC ATAACGAATA CCTCTTTTTT ATTTTAATA TTTGCTTGT TACAAACTTG	180
ACAAGTTAG TATAACAGTA TCTATTAAATT TTTTCATCC AAATCTGAA TTGGCATTG	240
AACGTCTTGA ATTAGTTTT TTGTTCAAAT ATCATCTCTA TTTTAAAAAA AGATGTTTTC	300
TAATCACTTT TTTACTATTT AGACTTCCTG CAAAACAGA ATCCTAGTTC ATGATTGATA	360
ATACCAGCAA TCAAATTCTAT TCGTAATCCG AAGCCTTAC GATGATTTCG ATAGGTTGTT	420
GAAAACATT TAAACGTTT TACTTTGGCA AAGATATTCT CAACCTTGCT TCTCTCCTTA	480
GATAGCGCAT GATTACAGGC TTTATCTCA ACTGTTAGCG GCTTGAGTTT GCTGGATTAA	540
CGTGGAAATT TGTGCTTGTAG GATATATCTT CATGAGCCCT TGATAACCAC TGTCAAGCCAA	600
GATTTTACCA GCTTGTCCGA TATTCTCAT TTCTAAAAC CATCTACTTC CGTTGACTTG	660
GAACCTCGAT TGCTATTTTC CTTGAATGAT TTTAACACCA TCTCCTACAC TTTGGAGTTG	720
GTCAATTCTC TCATCGCTGA TTTGATACT AAATTCTATCC TCCAGCGTCA AGATAAAACTC	780
CATCAAATCA ACTGAGTCAG CATCCAAGTC GTCTTTCAGA CTCAAGGATT CTGTCACGAC	840
AAAGTCCTCT CCCTGTGCT CTTGGATAAT GGTCACAATA CTGTCAAAAA TTTCTTTTTC	900
TCTCATCTCT TTTATTCTCC TGAAAATTCA CGCGCAGTCT GGGCAACTAC TTCTGTTCT	960
AGCATGGTAC GAATCTGGCG AATCGTACTA TAAACAGCCT TGGCATCGCT TGAGCCATGA	1020
GTCTTGACAA CAGGTGCCCT GACACCAAAAC AAGACCGCTC CACCAACATC TGAATAATTG	1080
AGCTGTTTT TCACACCTCT GAGGCTGTCC TTGAGAAGGA GGGCACCTAG TTTCGCTCGA	1140
AGACCACCACT CGTAAATAGC TGTCTTGAGC AAGCCCATGA TTCCCATAGC TGTCCCTTCG	1200
ATGGATTGAA GCACAGCGTT TCCCGTGAAA CCATCTGCCA CAACAAACATC TGCAACGCCA	1260
TTCATCAAAT CACGCGCTTC CACGTTTCCG ATAAAGTCA AACTTCTAC AGCCGCCAGT	1320
AATTCTAAAG TTTCTTACG AAGCGGGTCG CCCTTGCTAC TCTCTGTTCC GTTGTGAGC	1380
AAACCAACAC GTGGTTGCGC AATGCCACGA ACATTCTTGG CATAGAAAAGA ACCTAGGACA	1440
GCGTATTGAT GGAGGGTGTG GGCTGTATTT TCTGCATTAG CACCGAGGTC AAGCATGTCA	1500
AAACCTTCTC CATCTACAGT CGGCAATGTT GACATAAGTC CAGGACGGTC GATATTCTTG	1560
ATACGACCCA CGATGAAGAA TCCACCAAGCC AACAAAGCAC CTGTATTCCCC AGCCGAAAGG	1620

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ACAGCGTCTG CTTCACCATC TTTGACAGCC TTGGCTGCCA ATACCATACT GGCA	1680
TTATTCCGAA TAG	1693

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTAAATCTGC TTGCTTAGTC CACTTGCTTG AGCCAAGGAG TCACATACTC AAAATTTCA	60
TGAAAGTCAT AGGTACCGTC TTCTTTTTA GCTGAAAAGA AAAGTCCATC GTGGTAGAGC	120
AAATCCCCGT GGGCCATAAT TCTGGCAGTT TTTTCCTCTT CCTACTCCTG AGACTTTGC	180
TTAGTCCCCT CTTGAGAAAT AGTATCTCGT TTTTGACTAG TCAAGGGATT CCTTGGAAAGC	240
TTTCAAACAA CAAGACCAAG CCCATTGATA AACCAACTGC TAGCAAGAGT ATGCCACAA	300
ATCCCTTATT GCTCCACTTG CGATAACTCC TAAAAAGTTT ACCAAGCCCT TCATAAAACG	360
AAAAGCTAAA CCACCCGTAT TTGATTTTG TCTTCTTTGT ATCTTCGTT TCCTACTTT	420
CTTATGCAAG CCTTTCTTT TTATTATATC ACAGATAAGT ATTTCTTTCA CAATTGAATT	480
GAACCTCCCA TCTATTTCCT ATAATCCTA AATGCCATAA TGCTTCAAT TCCTGTCATT	540
TTGTGATATC ATGTAGAAGA AATGAACCAA TCCACAGTGG CTTATTCCAA GTATACCACT	600
GGGGCTTGG CAGTAG	616

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1973 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTAATATAGA ATAATCACCG CGCTTGTGAA AGAACGATTG GATGATAATC CAATCGTTCA	60
GGGAAATTGG AAGACCTTGG GTTCCAATT TAGGCATGAG ACACCTTTGG TGGCTGCTGC	120
CGTCCCTCAC AAGCTAAGGT GATTGTTGAA AAAGAGGAAA AAGGAGAAGA AATGAAACCA	180
GTAATTCCA TCATCATGGG CTCAAAATCC GACTGGCAGA CCATGCAAAA AACAGCAGAA	240
GTCCTAGACC GCTTCGGTGT AGCCTACGAA AAGAAAGTTG TTTCGACCA CCGTACACCA	300

GACCTCATGT TCAAACATGC AGAAGAAGCC CGTAGTCGTG GCATCAAGAT CATCATCGCA	360
GGTGCTGGTG GCGCAGCGCA TTTGCCAGGC ATGGTAGCTG CAAAAACAAC CCTTCCAGTC	420
ATTGGTGTGC CAGTCAAAGTC TCGTGCTCTT AGTGGAGTGG ATTCACTCTA TTCTATCGTT	480
CAGATGCCGG GTGGGGTGCC TGTTGCGACC ATGGCTATCG GTGAACCTTT TTTTAGGATA	540
TAAAACAGGG TTCGGATAAG TTTTTTGCA AGGTGGATGA TGGCTACATT GTAATGTTT	600
CCTTATTCTA ACTTAGTCTT AAGATAGGTC TTAAAACCAG GTGAAAAGCG AAGGCATGCT	660
TTGGCAGCTT GTATGAGTAC CTACCGCAGA TGAGGGAAC CCCGTTGAC CATCCTTCCA	720
ACTAAATCAA TCTGACCTGA CTGATAAATA GAAGAATCCA GTCCAGCGAA AGCTTGTAA	780
TGAGCAGGAT TATCAAAGGC ATGAATATTTC CGAACATCTCGG CTAAAATGAC CGCCCCCTAA	840
CGATTCTCAA TCCCAGTAAC CGTCGTGATG ACCGAGTTA ACTCAGCCAT CAAGTCATTG	900
ACACATTTC CCGCCTTGTG AATGAGCCTC TTGTAATGTT TGATGTTTC ATTACACGAG	960
ATAAAACGTC TATGCGTTAT CAAACTCATT ACCAATTAAA ACAAATGTGG TTAGATCCTT	1020
TCGGAAATTG TCAAGCGATT GGAGGAAATG AACTAATCCA CAGCGGCTTA TTCCAAGTAT	1080
ACCACTTGGG CTTTGGCAGT AGCTAACTGC GCTAAATATA ATATAAGGAG GAGTAAAATG	1140
AAGACAGTTC AATTTCCTTG GCATTATTTT AAGGTCTACA AGTCTCATT TGTAGTTGTC	1200
ATCCTGATGA TTGTTCTGGC GACTTTGCC CAAGCCCTCT TTCCAGTCTA TTCTGGACAA	1260
CGGGTGAACG AGCTAGCCAA TTTAGTTCAA GCTTATCAA ATGGCAATC CAGAACCTTGT	1320
ATGGCAAAGC CTATCAGGAA TTCATGGTCA ATCTTGGCCT GCTGGTTTG GGGTCTATTT	1380
ATCTCTAGGT GTAATATAAA CATGTGTCTC ATGACGGCG TGATTGCAGA ATCGACCAAC	1440
GAGATGCGCA AAGGCTCTT TGGTAAGCTT GCTCAGTTGA CGGTTTCTTT CTTTGACCGT	1500
CGACAAGATG GCGATATCCT GTCTCATTTT ACCAGTGATT TGGATAATAT CCTCCAAGCC	1560
TTAACGAAA GCTTGATTCA GGTCTATGAGC AATATTGTT TATACATTGG TCTGATTCTT	1620
GTCATGTTT CGAGAAATGT GACGCTGGCT CTCATCACCA TTGCCAGCAC CCCATTGGCT	1680
TTCCTTATGC TGATTTTCAT CGTAAAATG GCACGTAAT ACACCAACCT CCAGCAGAAA	1740
GAGGTAGGAA AGCTAACGC CTATATGGAT GAGAGCATCT CAGGCCAAA AGCCGTGATT	1800
GTGCTAGGAA TTCAAGAGGA TATGATGGCA GGATTTCTTG AACAAAATGA GCGCGTGGC	1860
AAGGCAACCT TTAAAGGAAG AATGTTCTCA GGAATTCTTT TCCCTGTCTA GAATGGGATG	1920
AGCCTGATTA ATACAGCCAT CGTCATCTT GCTGGTCGG CTGTACTTTT GAA	1973

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTAAACCAAT AGTTGCTGAA GACCATAATC CAGCTGCTGT TGTAAACCT TTAACCTTTT	60
GATTAGTTAC CATGATTGTT CCTGCCCTA GGAAACCCAA GCCACTAATT ACTTGGGCTC	120
CCATTGACT AGGATCACCG CTACCATCAC GACTAGTGAT GAACTGATT GTCTATCATTA	180

CAACACAAGT TCCCCAACAA ACTAGTAAGT AGGTTCTAAT CCCTGCTGCT TGGTTTTG	240
CTCCTCGCTC ATAGCCAACA ATGCCACCGA AAAGAATCGC TAAAAAGCAC CTAAGAAGTA	300
TTTCCCAAAT ACTCAGTTCG TATGAAAGAT TCATATTATC TCCTACCTCG TTPACCTTGG	360
AATAGGCTTG ATAAATAAAG AGCTGCACTA GACATAATCA TTAAAATTAC AGAATAAAC	420
AACATCATTG CCTGTGCATT TAAAGTTGCT GTTTCATCG TAGACTGTTT AATAACGATT	480
CCCAATGGTT GGAAAAGTGG ATGGTACAAG AATACAGATA AGTCATAGTC AGATAATAAA	540
GAATTAAAGT TTAACACAAAC TACTGATAAT ACGACTGGTA AAATATAACGG TATAATAACT	600
CGCACCATAG TGTAGAACT AGATGCACCC ATACTACGTG CAGCTCTTC CATATCATT	660
TCTATACTGA AAAATACAGC CCGAATCATT CTATAAGAAA ATGGTAATT TTGAATAGTA	720
TATGCAATAA GTAAAATAAT TACTGTTCCCT ACTAAAACATA AATTAAATAG TATTAATGA	780
GGTATATTAT AAGTGAACAT TAATCCTAGT GCAATCAATG TACCTGGAA TATCCATGGT	840
ATCAGTGCAC CATACTCAAA GAATTTATCG AACTTACTCT TGTTTTATG TACAATACGT	900
GAAATTACTA TTGCTATAAT TGTAGCAATT ACCGCAGCTA AAATTGCATA AACAAACGCTG	960
ACTAGGTAAG GACGAAATGA TTGAGCATCT GTAAATAAT TAGCATAGTT CGCTAACGTA	1020
AATTAGATA GATCTAAAGT TCCCCTTGTG ATCGTCAACG AGTCTGTAAA CGAGTATAGA	1080
ATTATCAAAA CTATTGGTAA CATATAGATT GCAAACAATA CATAACGAGC AATGTGAGCA	1140
AGAATTATTC CATAATGGAG AAGAAAATTA TCTGCTTCCT TAATACTAGC CTGGTTTTCG	1200
AAACAGAAT	1209

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTAAGTCCTT TTAGTTTAT CTTAATTCTC TTATTGTTGT AATAATCAAT ATAGTCTATA	60
ATGGCTTGT CCAATTGCTT AAGCGACTGA AACGACTTCT CATAACCGTA AAACATTTC	120
GATTTCAGAA TCCCAAGAA AGATTCCATC ATACCGTTGT CTTGGCTGTT TCCCTTGC	180
GACATAGATG CTTGAATTCC CTTACTCTTA GGAACCGATG ATAAGAATCG TGTGGTATT	240
GCCAGCCTTG GTCACTATGG AGAATCGTAT TCTCGTAGTG CTTCTCTGTG AATGCCTGTT	300
CCAACATTGT TTGTAATTGT TCTAAGTTGG GTGAAGTTGA AAGATTATAG GCGATAATT	360
CGCTATTAAA GCCATCTAAA ACTGGTGATA AGTAAAGCTT TTGAGTACTT GCTGGAATGG	420
CAAATTCTGT CACATCTGTG TAGCACTTTT CCATTGTTT AGAGCCTTC AATTGGCCTT	480
GAATGAGATT CTCTGCCTTC TTACCAACGT CTCCCTTATG AGAAGATTTC GTTCTGTG	540
CATTTAGCT TGTAAATTGA GTACTTTCAT CAAGCCTTGA ACTCTTTAT GATTACCAG	600
ATAAGCACGA TTCCCTTAGTT CTAATGAAT ACAGCGATAA CCATAATTTC CCTTGTGTT	660
GATAAAAATG GATTGAATT CAGCTTAAAG CTCTTGGTCC TTATCTGGTT TGTNTAG	717

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTAAATCAC	AGATTAAACC	AAGTCGAGA	TACGGCCTGG	TGTTCCAATA	ACAATATGAG	60
GCTGATTGCT	TGCCAATTTC	TCAATCTGGC	GAGCCTTATC	CGTACCACCC	ACATAATTAA	120
CCACACGAAC	TCGACATCT	GAGTGAGCTG	AAATCTGACG	CGCTACTTGG	AAAATTGAG	180
TAGCCAAC	TCGACTCGGT	GCAGTAATCA	CTGCTTGAC	ACTATCGCTA	GCTTCATCTA	240
ATTGCTGGAA	AATCGGTAAC	AAGAAAAGTAT	GAGTCTTACC	TGAACCTGTT	TTTGATTCTC	300
CTACTAGGTC	ACGACCTGCC	AAAACAATAG	GAATCAACTT	GTCTTGCACC	TCTGTTGGAG	360
TTGTAAATT	AACTCCTCC	AAGGCTTCTC	TAATATAGTT	TTTAAATTGA	ATTTCGTAA	420
ATGACATAAC	ATCCTCGATT	CTATCTATCT	TATCAATTAT	ACCATATTTT	ATTCCATTAC	480
AGTAGTCTCA	CTTATTTAGG	CTATTTCCAG	TAGCTTCTCT	AGTAAGAAAA	GGCTGGAATT	540
TTATAGTTCC	AACCTCTTT	CAGTTATTAT	TTCCAGTTTA	ACATAGCATT	CAAGCCATAG	600
TGATCACTCA	CTTGTGGACT	CTTGTACCA	TCAAATACGA	CATGAAATT	TTCCACCGCT	660
AACTCTTGG	TAGTAAAGAC	ATAATCGATT	CGAAGGGTT	CAGTGTCCC	TTTCCAGCCA	720
TCAATTTCA	GCAGAACAGT	ATAGCTACCA	CTTTCTCTT	GAGCAACTTC	AAATGCGTCT	780
TGTAAGCCTA	ATGGACTAGC	AAAATAGCT	TGGTAACCTT	CCCTGACCTG	CTGGGTTGTT	840
AAAATCTCCA	G					851

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTGTTGAGAT	TGTTACGAAA	TAAC TGAGAA	TATTTAAGGA	GAAAATATAT	GTGAAACAC	60
TTAAACTTAA	AAGGTCACTT	ATTGACAGCC	ATTT CCTATA	TGATTCCAAT	TGTTTGTTG	120
GCAGGATTCT	TAGTTGCCAT	TGGTTTAGCA	ATGGGGGGTG	GTGTTCTGTA	CGCTCTTGTA	180
GCAGGAAAAT	TCACTATCTG	GGATGCTTTA	GCAACTATGG	GTGGTAAAGC	CCCTGGTCTC	240

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TTGCCAGTTG TTATTCGCTAC AGGTTTGTCT TACTCGATTG CTGGTAAGCC AGGGATTGCA	300
CCAGGTTTTG TTGTTGGTCT AATTGCCAAT TCTGTTGGTT CAGGGTTTAT CGGTGGTATC	360
TTGGGAGGTT ATATAGTTGG TTTCTTGGTT CAAGCGATTA TTAAAAAGGT CAAAGTACCA	420
AACTGGATTA AAGGTTAAC GCCAACCTTG ATTATTCCTT TTGTACCTCT TTGTTAAGTA	480
GTTTGATTAT GATTATATT ATTGGGGCGC CTATCGCAGC CTTTACCAAC TGTTGACGA	540
G	

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTGGAATGAG TGTATAAGCC CAGCCCAAGT TTTGCATCCG TTCAAAGTTC CAAGACCCCTT	60
GTAAGAAGGT TGAACGCCAC CAAACTTTT TACGATCTGA TTTAGTTAAT TGAAGTTTTT	120
CAGTCATGAT GTTTTCAGTC CTTTCTTATC TTAGTAGTCT TCTAGGATAT CGCCGATTGG	180
GTCGTTAGAA GTTGCGGCTC CTCCGCCACC ATTTCCACCA GTTTTAGAAA GGTGAAGGTA	240
GATAAGAGCG ATAGCAACAC CGATAGCACC GAATCCGATT AGAGTAATAT CTGACACAGC	300
AGCGAGAACG AAACCAAGAG CGAAGAATGG CCATACTTCA CGAGTTGCCA TCATGTTGAT	360
AACCATGGCG TAACCAACGG CAACGACCAC ACCACCACCG ATAGCCATAC CATCTTGAG	420
CCAGTCTGGC ATGGCACTAA GGATACTTTC TACAGTTTCA GTTGGTACCA TAAGGAGAAG	480
AGCTGCAGGA AGCGCGATAC GAAGTCCTTG GAAAAGTAGC GCAATGAAAT GGCACGCTC	540
CACAGCGCCG AAGTCACCTT TTTAGCGGC AGCATCTGCA GTATGAACCA AACCAACTGA	600
AATTGTACGA ACAATCATTG TCAAGAAAAG TCCAGCTACG GCAAGAGGGA TAGCAACCGC	660
TTGGGCAACA CCGATACCAAG TCTTGGTAAA GTCACCACCA AGAACCATGA TAATGGCAGC	720
AGCGACAGAA GCAAGTGCAG CATCAGGAGC GATAGCAGCA CCGATATTG ACCAACCAAG	780
GGCAATCATT TGAAGCGATC CACCGAGGAT AATCCCTGCT TCCAAGTGGA CCTGTTACAA	840
GCCCAATAAG GGTACAGGCT ACAACTGGTT GGTGAAATG GAACTGGTCG AGGATGCCTT	900
CAAGACCTGC AAAGGAAGGC TACAACGACT ACTAAAACCA TAGAAATAAT AGACATGTTT	960
AAAATCCTTT CATAAAATAAT GGCTTATTTG ACATTGGCTT TGTTAATCAA GTCAAACAAA	1020
TCTTTTTAG AATCATTGG TACTTTACGG ACATCAAATT CAACACCCAA GTCACGCATT	1080
TTTTCAAATG TAGCAACATC TTCTTIGTCC ATAGACAAAA CGGTATTGAC CAATGTTTA	1140
CCTGTTGAGT GAGCCATAGA ACCAACGTTA AGAGTCTGTA TTGGCACGCC GCCTTCGATG	1200
GCACGAAGGG CATCTTGAGG TGTTCAAAC AAGATAAGGG CATGTGTTTC TCCAAAACGT	1260
GGGTCTTTG AAATATCAAT CAGTTTTGAA ATTGGAACCA CGTTAGCCTT GACATTACCT	1320
GGAG	1324

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCATAAGGAA GCTGTCGCTC GTTCCGCTAA GGTATGGACA CCACCGTGAA CATTGGCATT	60
GTCCTGCTCA TAGTAACTGT TAATAGCTTT CAGAACTACT AGTGGTTTT GTGTCGTCGC	120
AGCATTGTCC AGATAGACCA GAGGTTCATC ATTGACAATC TGATCTAAA TTGGAAAATC	180
CTTGCAGAAC TCCTCTACAT CTAACATAGG CTTCCCCCTTA GCGTTTGAC AATTTCTCTT	240
CGATAGTTGC AATCATTTCA TCACGAACCTT CCTTGACTGG AATCTCCACG ATAACAGATC	300
CAAGGAAACC ACGAACAAACC AAACGCTCTG CAGTTGCCCT ATCCAATCCA CGACTCATGA	360
GGTAATACAT GTCCTCTGGA TCAACTTGTC CGATAGACGC TGCCTGTCCT GCAGTGACAT	420
CATTTTCATC AATCAAAGA ATGGGGTAG CATCTGAACG CGCTTGGCTC GAAAGCATGA	480
GAACACGGCT CTCTTGTGTC GCATCTGCTC CCTTAGCACC CTTGATGATG TGGCCGATAC	540
CATTGAAAGT CAAAGTTGCT TTTTCAAGGA TAAACCCATG TTGTAGGATA TTTCCGATAG	600
AGTTGCAGCC ATAGTTAGTT ACACGAGTAT CAATCCCTTG TACCTGACGA CCACTTGAAA	660
GAG	663

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 649 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTAGTTGGAT GGCTTCAATA AAGGATGATT TGGCTGCTCC ACTATTGGCA ATGAGCTGAA	60
AACAGATATA TTCCATTCTC TCGTCATCTT ATTTCTCCTA TCCATTCAG TGCTTGGTCC	120
AGAACTTTTG CTCCATTCA CATTCCGTA TCCCAGATAT CAATGGTATC TACAGGGATA	180
TTTCCTGCAA TTTCTTCAC AGCAAGTAAC TCATAACGAA TTTGTGGCCC AATTAGAATG	240
ACATCTGCTT CATGGATATT CTTTTTAGCT TCTGTCATTG ATTTTGCTTG GATAGAAATT	300
TCAATCCCAC GTTCAGTCGC ACTTTGTTGC ATTTTTTAA CAAGCATACT TGTCGACATT	360
CCCGCATTAC ATACTAATAA AATTGTTTC ATAATCTTAA CCTTCATTT CTTGTTCAAC	420
AACTTTGTCA TTAACTTGA TAAATGGAAT GTATAGAAC ACTCCAAGTG CAAAGATGAT	480

GAATTGAACT AGAACTGCTC TCACGTCCCC TGCTGTTGCT AACCATGCAT TTAAGAATAC	540
TGGTGTAGTC CAAGGAACCT GTATAAATGC AGGACTCATG AATCCTGTAA CTGTTGCTAA	600
GTAGCTGATT AAAATACCAA GGACTGGAAC TGTGATAAAAT GGAATAGTC	649

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTTGGTATTAA TTTGAAATCA GATGGTTCTT ATGCAAAAAA TGCATGGCAA GGAGCTTATT	60
ACCTTAAATC AAACGGTAAA ATCGTACAAG GTGAGTGGGT TTATGATTCT TCTTACCAAG	120
CCATGGTATT ACTTGAAATC AGATGGTTCA TATGCTCGCA ATGCATGGCA AGGAAACTAC	180
TATTTGAAAT CAGATGGTAA AATGGCTGTC AATGAATGGG TTTATGATGC CACCTATCAA	240
GCATGGTATT ATTTGACATC AGATGGTTCT TATGCTTACA GTACATGGCA AGGAAATTAC	300
TATCCTAAAA TCGGATGGTA AAATGGCTGT CAATGAATGG GTTGATGGTG GACGTTATTA	360
TGTTGGCGCT GACGGAGTTT GGAAGGAAGG TCAAGCAAGT ACAGCTCTC CTAGTAATGA	420
TAGCAATAGT GAATATTCT GCTGCTTTAG GAAAGGCAA AAGTTATAAT TCGTTATTCC	480
ACATGTCAAA AAAAACG	497

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTAGTCTAAA TTTTTAAAAA CAAAGGTCAA AGATAGTCAA TATCAGTAAT CATAACTAAG	60
TAAACAAAAAA GAGGTAAGA ATATGAATAA CAACTTTAAT AATTTTAATA ACATGGATGA	120
TTTATTTAAC CAATTGATGG GTGGTATGCG AGGATACAGT TCTGAAAATC GCCGTTACTT	180
AATTAATGGA CGCGAAGTCA CACCTGAGGA ATTGTGTCAC TATCGTACGA CTGGTCAATT	240
ACCAGGAAAT GCAGAAACTG ATGTGCAAAT GCCACAAACAG GCATCAGGTA TGAAACAAGA	300
CGGTGTCCTT GCAAAACTAG GTCGAAACTT GACAGCAGAA GCGCGTGAGG GCAAGTTGGA	360

TCCTGTTATC GGACGAAACA AGGAAATTCA AGAACACATCT GAAATCCTCT CACGCCGCAC	420
CAAGAACAAAT CCTGTTTGG TCGGAGATGC AGGTGTTGGT AAGACAGCAG TTGTCGAAGG	480
TCTAGCGCAA GCCATTGTGA ACGGAGATGT TCCTGCTGCT ATCAAGAACAA AGGAAATTAT	540
TTCTATTGAT ATCTCAGGTC TTGAGGCTGG TACTCAATAC CGTGGTAGCT TTGAAGAAAA	600
TGTCCAAAAC TTAGTCAATG AAGTGAAGA AGCAGGGAAT ATTATCCTCT TCTTTGATGA	660
AATTCCACAA ATTCTTGGTG CTGGTAGCAC TTGTGGAGAC AGTGGTTCTA AAGGGCTTGC	720
GGATATTCTC AGCCAATCGA TCTCTCTCGT GGAGAATTGA CAGTGATTGG GGCAACAACT	780
CAAGACGAAT ACCGTAACAC CATCTTGAAG AATGCTGTC TTGCTCGTC TTTCAACGAA	840
GTGAAGGTCA ATGCTCTTC AGCAGAGAAT ACTTTTAAAA TTCTPTCAAGG CATTCTGTGAC	900
CTCTATCAAC AACACCACAA TGTCATCTTG CCAGACGAAG TCTTGAAGC AGCGGTGGAT	960
TATTCTGTTC AATACATTCC TCAACGTAGC TTGCCAGATA AGGCTATTGA CCTTGTGAT	1020
GTAACGGCTG CTCACTTGGC GGCTCAACAT CCAGTAACAG ATGTGATGTC TGGTGAACGA	1080
GAAATCGAAA CGGAAAAGA CAAGCAAGAA AAAGCAGTTG AAGCAGAAGA TTTTGAAGCA	1140
GCTCTAAACT ATAAAACACG CATTGCAGAA TTGGAAAGGA AAATCGAAA CCACACAGAA	1200
GATATGAAAG TGACTGCAAG TGTCAACGAT GTGGCTGAAT CTGTGGAACG AATGACAGGT	1260
ATCCCAGTAT CGCAAATGGG AG	1282

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTTGATATAA TTCTTGTTC GAAAGATTCT CCTTAGGTAT ATCTATTCTT CCACTAGTAA	60
ACGGTAATTC CAAAACAGAG TTTACTTCGT TAAATGTAAG CCAATATTAA ACTTTATCTT	120
TATACCTTTC TAAAACGTGTT CGAGCAAATT TTTCATAAAAA ATGAATCATT CTTCTATCA	180
ATCCATCCAT GATATTTCCT TGCTAAATAT AATGGAGTCT CATAGTGTGA AAGAGTTACA	240
AGTGGTTCTA TCCCCGTGAGC ATGTAGTTCA TCAAACAAATT CATCATAATA TTTCAATCCA	300
GCTTCGTAG GTTCTTCCTC ATCTCCTTTT GGAAAATTC TACTCCATGC AATAGAAGTA	360
CGAAAACAT TAAAGCCCAT TTCAGAAAAC AAGGATATAT CTTCTTATA TTTATGATAA	420
AAATCAATAC CTATCAATTAA TAAGTTATCT TCTGTAGGAT TTTCTGTGTC TTCTCTAAT	480
CCACCTTGG GTAACACATC CTGAACACTG AAGCCCTTAC CATCTTCATT ATATGCTCCC	540
TCTACTTGTAT TAGCTGCAAC AGCTCCACCC CAAAGAAAAT CATCTGGAAA AATGGTCATA	600
ACTTTCTCC ATTATAATAT TACCAAGTAAT TCCCTAGAAA TGCTCGATTG TCTGATTATT	660
AGGTAATATT AATACATCTA GAAAATCATT GGTATTGTT ACAATTACTG GTGTAACGT	720
TTCTGTGCT TTAGTCTTGA TTAATTCAA GTCCATTCA AAAATCAACT GATTTTTGAA	780
AACTCTGTCT CCTTCTCTA CATGACTAAT AAAACCTTGA CCTTTTAG	828

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AGCTATGGTC AGACTCAGAT TGATGGCGTT GCTTATGCCA AGTACGATAT CTTCCGTTTA	60
AAGAACGGGA AAATTGTGGA GCATTGGGAT AATAAGGAAG TCATGCCCAA GGTAGAAAGAC	120
TTGACCAATC GAGGGAAAGTT TTAAATTGAG GACAAAGAAT GATTGAATAC AAAAATGTAG	180
CACTGCGCTA CACAGAAAAG GATGTCTTGA GAGATGTCAA CTTACAGATT GAGGATGGGG	240
AATTATGGT TTTAGTAGGG CCTTCTGGGT CAGGTAAGAC GACCAGCTC AAGATGATTA	300
ACCGTCTTTT GGAACCAACT GATGGAAATA TTTATATGGA TGGGAAGCGC ATCAAAGACT	360
ATGATGAGCG TGAACCTCGT CTTCTACTG GTTATGTTTT ACAGGCTATT GCTCTTTTC	420
CAAATCTAAC AGTTGCGGAA AATATTGCTC TCATTCCTGA AATGAAGGGG TGGAGCAAGG	480
AAGAAATTAC GAAGAAAACA GAAGAACTTT TGGCTAAGGT TGGTTTACCA GTAGCCGAGT	540
ATGGGCATCG CTTACCTAGT GAATTATCTG GTGGAGAACAA GCAACGGGTC GGTATTGTCC	600
GAGCTATGAT TGGTCAGCCC AAGATTTTC TCATGGATGA ACCCTTTTCG GCCTTGGATG	660
CTATTTCGAG AAAACAGTTG CAGGTTCTGA CAAAAGAATT GCATAAAAGAG TTTGGGATGA	720
CAACGATTTT TGTAACCCAT GATA CGGATG AAGCCTTGAA GTTGGCGGAC CGTATTGCTG	780
TCTTGCAGGA TGGAGAAATT CGCCAGGTAG CGAATCCCGA GACAATTTTA AAAGTGCCTG	840
CAACAGACTT TGTAGCAGAC TTGTTGGAG GTAGTGTCA TGACTAATTT AATTGCAACT	900
TTTCAGGATC GTTTTAGTGA TTGGTTGACA GCTACAATGA CATTGGTCGG TTCCCTTGAGC	960
AAGAGATAGA TTAGCCAGAC AGTCATGCCA AAAATCCCTC CAGGTAAGAG CATAGACCGT	1020
TGCA CACATTA GTACGATTAA AAAAGTGATA ATGGCAAGAA AACTTGCTAC TGCTTGTAA	1080
AAAAAGGTTG TTAGTGTCA ATTAGTCAT CAATACCAAG GCGACAGAAAG TTCCCTGCC	1140
TAAAGCGAGG GTAATGAGCA GGGATTCAA CATCTTACTC ATACCAGAGT TTATGTGGTT	1200
GGTCATAATA TCACGGACCG CATTGGTCAA GGCAATACCT GGTACAAACG GCATGACCGC	1260
ACCAGCTATA ATCAAATCCT GCCCGTTTGA ATGGAAAAAC CCTGTGTTAG CCGAGCCCCA	1320
AAACTGGGGC CAATTATCC CCCAAAGACA AAAGCTCCAT CAAAGGCTGT CACAAAGGGA	1380
ATTGGATAAA ATTTTCCACA TAGAAGGAAA AGGCAAAACC AAATAAGGTC GCCACTCCTG	1440
CCCCAAGTGC TCGTAAATAT TCCGCT	1466

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AAGGTTCTTC	GTAAATGTAC	ACCATTGGAA	TGCTCAAAAT	GGGTTCTGAA	GCTGCTGCTA	60
AATCTGCACA	AGAACACGGT	CTTAAATCAG	TTGAAGTTAC	TGTAAAAGGT	CCAGGTTCTG	120
GTCGTGAGTC	AGCTATPTCG	TGCCCTTGCT	GCCGCTGGTC	TTGAAGTAAC	AGCAATTCTG	180
GATGGGACTC	CAGTGCCAAC	ACAATGGTGC	TTCGTCCTCC	AAAACGTCGC	CGTGTATAAT	240
CATCGCATTA	CACTGCTTTT	CGTTTAAGAG	GGAGTAACTA	AATGATCGAG	TTTGAAAAAC	300
CAAATATAAC	AAAAATTGAT	GAAAATAAAG	ATTATGGCAA	TTAGTAATC	GAACCACTTG	360
AACGTGGCTA	CGGTACAGCT	CTTGGTAACT	CTCTTCGTG	TGTACTTCTA	GCTTCTCTAC	420
CAGGAGCAGC	TGTGACATCT	ATCAACATTG	ATGGTGTGTT	ACATGAGTTT	GACACAGTTC	480
CAGGTGTTCG	TGAAGACGTG	ATGCAAATCA	TTCTGAACAT	TAAAGGAATT	GCAGTGAAAT	540
CGTACGTTGA	AGACGAAAAA	ATCATCGAAC	TGGATGTTGA	AGGTCTGCT	GAAGTAACAG	600
CTGGTGACAT	TTTGACAGAT	AGCGATATTG	AAATTGTAAA	TCCAGATCAT	TATCTCTTTA	660
CAATTGGTGA	AGGTTCTTCT	CTAAAAGCGA	CTATGACTGT	TAACAGTGGT	CGTGGATATG	720
TACCTGCTGA	TGAAAATAAA	AAGGATAATG	CACCAGTTGG	AACACTTGCT	GTAGATTCTA	780
TTTATACACC	AGTTACAAAA	GTCAACTATC	AACTGGAACC	TGTCGTGTA	GGTAGCAATG	840
ATGGTTTCCA	CAAATTAACC	CTTGAATCT	TGACAAATGG	AACAATTATT	CCAGAAGATG	900
CTTTAGGGCT	TTCAGCACGT	ATTTTGACAG	AAACATCTGA	TTTGTGTTACA	AATCTTACTG	960
AGATTGCTAA	GTCAACTGAA	GTGATGAAAG	AAGCTGATAC	TGAATCTGAC	GACCGTATTT	1020
TAGATCGTAC	GATTGAGGAA	CTGGACTTGT	CTGTGCGTTC	ATACAACGTG	TTAAAACGTG	1080
CCGGTATCAA	TACTGTGCAT	GATTGACAG	AAAAATCTGA	AGCAGAGATG	ATGAAAGTAC	1140
GAAATCTTGG	ACGCAAGAGT	TTGGAAGAAG	TGAAACTCAA	ACTCATTGAT	TTGGGTCTTG	1200
GATTAAAAGA	TAAATAAAGG	AGGAATACAT	GGCTTACCGT	AAACTAGGAC	GCACTAG	1257

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTATTGAAAC	AAGAAAAATA	GAGAATCPAA	GAAAGAGAAC	TTATGAATAT	TCAAGAAGAA	60
ATTAAGAAC	GTCGTACCTT	TGCCATTATC	TCCCACCCGG	ACGGGGGAA	AACAACCATC	120
ACTGAGCAGT	TACTCTAACT	TTGGGGGTGA	GATTCGTGAG	GCTGGTACGG	TAAGGGAA	180
GAAAACAGGG	ACTTTTGCTA	AATCTGACTG	GATGGATATC	GAGAAGCAAC	GTGGGATTT	240

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TGTTACTTCA TCTGTTATGC AATTGACTA CGACGGCAAG CGCGTGAATA TCTTAGACAC	300
GCCAGGGCAC GAGGACTTCT CAGAAGATAC CTATCGTACC TTGATGCCG TGGATGCTGC	360
GGTCATGGTC GTGGACTCTG CCAAGGGAT CGAGGCTCAA ACAAAAGAAAT TGTTTGAGGT	420
TGTGAAACAT CGTGGCATTC CAGTCTTAC CTTTATGAAC AAGTTGGATC GTGACGGTCG	480
TGAGCCTTG GATCTCTTGC AAGAATTGGA AGAAATCTTG GGCATTGCTA GCTACCCSTAT	540
GAACCTGGCCT ATCGGGATGG GGAAAGCCTT TGAGGGCTTG TATGACCTCT ATAACCAACG	600
TTTAGAGCTT TACAAAGGGG ATGAGCCTT TGCTAGCCCT AGAAGATGGA GACAAACTTT	660
TTGGTAGCAA TCCTTCTAC GAGCAAGTCA AGGATGACAT TGAGCTTTA AATGAAGCTG	720
GGAATGAGTT TTCAGAGGAA GCTATTCTGG CTGGAGAATT GACGCCCTGTC TTTTCGGTT	780
CAGCCCTGAC AAACCTTGGT GTGCAGACCT TCCTTGAAT CTTCTCAAG TTTGCTCCAG	840
AACCACATGG TCACAAGAAA ACAGACGGTG AAATTGTTGA TCCTTATGAC AAGGATTTCT	900
CAGGCTTGT CTTTAAAATC CAAGCCAACA TGGATCCTCG TCACCGTGAC CGTATTGCCT	960
TTGTCCGTAT CGTATCAGGC GAATTGAGG TGAGGATGAG TGTCAATCTC CCTCGTACTG	1020
GTAAGGGTGC CAAACTATCT AATGTTACCC AGTTTATGCC GGAGAGTCGT GAGAATGTGA	1080
CCAATGCCGT AGCAGGTGAT ATTATCAGGGG TTTACGATAC CGGTACTTAT CAGGTTGGGG	1140
ATACCTTGAC GGTTGGAAAA ACAAGTTTG AATTGAAACC ACTGCCAACC TTTACTCCTG	1200
AAATTTTCAT GAAAGTTCT GCTAAGAATG TTATGAAGCA AAAATCCTTC CACAAGGGGA	1260
TTGAGCAATT GGTGCAAGAA GGAGCCGTT AGCTTTATAA GAATTACCAA ACAGGTGAGT	1320
ACATGCTGGG AG	1332

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 932 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TTGGACGCTG GAACAAATCC AAGCTGACCT GTTCCAAGAC CAGACTTGGT ATGCTCTGGC	60
TTATGATGGG GCAGAACTGA TTGGCTTCTC AGCTGTTCAAG GAGACTCTTC TTTGAAGCAG	120
AAGTCCCTGCA AATCGCTGTC AAAGGAGCCT ATCAGGGTAA GGGCATTGCG TCAGCCTTGT	180
TTGCTCAATT CCCGACAGAC AAGGAAATT TCCCTCGAAGT CAGACAGTC AATCAACGAG	240
CGCAAGCATT TTACAAGAAA GAAAGATGG CAGTTATCGC TGAGCGAAAG GCCTACTACC	300
ATGACCCAGT CGAGGACGCC ATTATCATGA AGAGAGAAAT AGATGAAGGA TAGATATATT	360
TTAGCATTG AGACATCCTG TGATGAGACC AGTGTGCGCG TCTTGAAAAA CGACGATGAG	420
CTCTTGTCGA ATGTCATTGC TAGTCATTGAG GAGAGTCACA AACGTTTTGG TGGCGTAGTG	480
CCCAGTAG CCAGTCGTCA CCATGTCGAG GTCATTACAG CCTGTATCGA GGAGGCATTG	540
GCAGAAGCAG GGATTACCGA AGAGGACGTG ACAGCTGTTG CGGTTACCTA CGGACCAGGC	600
TTGGTCCGAG CCTTGCTAGT TGTTTGTC GCGGCCAAGG CCTTTGCTTG GGCTCACCGGA	660
CTTCCACTGA TTCTGTTAA TCACATGGCT GGGCACCTCA TGGCAGCTCA GAGTGTGGAG	720

CCTTTGGAGT TTCCCTTGCT AGCCCTTTTA GTCAGTGGTG GGCACACAGA GTTGGTCTAT	780
GTTTCTGAGG CTGGCGATT A CAAGATTGTT GGAGAGACAC GAGACGATGC AGTTGGGGAG	840
GCTTATGACA AGGTCGGTCG TGTCAATGGGC TTGACCTATC CTGCAGGTG TGAGATTGAC	900
GAGCTGGTC NTCTNGGGCA GGANATTTAT GA	932

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTAAACTTTC GCTCATAGGC ATACAAATT A ATCCTTTGGC ATAAGTAGCC ATAAAATTAA	60
CATTTTCTGT TGTAGCTGCT TGTGCAGAAC AAATTAAGTC TCCTTCATTT TCTCTATCCT	120
TGTCGTCTAT AACAAAGAAC A AGTCGTCCCT TCTGCAATGC TTCTAATGCT TCTTGTATT	180
TTCGATATTC CATTGACTGA TTATCCTTTC TGCTAAAATC CATTGGATA TAATAGTTCC	240
TTCGATATTT CTGATTTGG AGAGTTATCC ATCAGTTTT GCACATATTT ACCTAAGATA	300
TCATTTCAA GATTACTGT ACTCCCGACT TGTTTACTCT TAAGAATGGT TTGTTCAAG	360
GTATGAGGGA TAACAGATAC TGAAAAGTTT ACTTTGGAGA CTTTAGCGAC AGTCAGACTA	420
ATGCCGTCAA TTGTAATAGA TCCCTTTCA ACTATTAAAT CTAAAATTTC TTTTGTGTG	480
TTGATTTGAT ACCATACAGC ATTATCATCT TTTTTTATG ACGAGATTTT TCCTGTACCA	540
TCAATGTGTC CTGTAACGAC GTGACCCCCA AGTCGACCGT TGACAGATAA GGCTCTTCT	600
AGATTCACCT CACTTCCATG TTTTAATAGA GTAAGAGCTG TTCGACTCCA TGTTTCATTC	660
ATTACATCAA CTGTAAGGA TTGATGATTG AAATGAGTAA CTGTAAGACA GATACCATT	720
ACTGCTATAC TATGCCCTAA ATGGATATCC GTTAATATTT TTGAGGCTTT AATTGATAGT	780
TTACAATTAC GAGAGTCTTT CTGTATTCCT TCAACTTTTC CGATTCTTC AATTATTCCT	840
GTGAACATGG ATAAATCACT TCACTTTCTA TGAGATAGTC NTTCCCTNTT TGAGAAAAAG	900
CATAAGGTTT CAATCTAATA GCGTCATTG GCAAAGAAAT GCCTTCACCT CCGACAGGAA	960
ACTTGGCACT GCCTCCAAAA ATTTTGGTG CAATATATAT TTTCAGCTCA TCAACAATT	1020
GTTGTTCAA AGCACTCCAA TTCATTAGAC TGCCCCCTC TACAACTAGG CTATCAATCT	1080
GCATGTTCC TTAGATGTTN GCATTAAACT CNGATAAGTC TATATGATTG CCTTTTTCT	1140
TTATGGAAAG TATTCCCC	1158

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TAAAGGCTGT TTGGATAATG TAACATAAAG AAATCTTGTT TAGCAGGGAT TGAATAGAGT	60
TCCTGAAGTG ATGACTTCTT TATTAGACAT AATGTCTGGA CCCAAGATTA AAAGAACATGGC	120
CCCGAAGAAT ACGAGCATCA AAGGTAGCAG ATGCAACAAAC TGTATCGTGG AAGATTGAGA	180
GGAACCTTAGG TAATTAAAGA TTGTCTAAC CTTCTCTTT CTTACCAAAG CGTCCTGCTA	240
CTTATCTAC AAACCAAGATT GCAAATTGCT GTGGGTGACC AATCGCAAAT CCGCCACAC	300
CAGTCAGCG TTGAGTTGCC TCAACAGTC AATTGAACT AACTGCCAG TAAAGTCCAC	360
AGATGATACC AATCGCTGCT GTACCGTAAG CATTGCGCAA TTGTGGTACT AAGAATAGAA	420
CCATAAGAGA TACTGTTGCA GCTAGCCATG CTGATCAATT CCCTCAACCA GTCCTATATC	480
TCAGCCAAGA GAATCGAGGA GGTCTTGCG GAATCTCCC AAAACATCCA TTCAGAATTA	540
GAACAAAAGC AAGTTACCAAG TGTCGGGTT TTACAAGTCC AAGAATTGAC TTTTACCTAT	600
CCTGATGCGG CCCAGCCTTC TCTGAGAGAC ATTTCCTTTG ATATGACTCA AGGACAAATC	660
CTTGGTATCA TTGGGGGAC TGTTCTGGT AAATCAAGCT TGGTGCAACT CTTACTTGGA	720
CTTTATCCAG TAGACAAGGG GAACATTGAC CTTTATCAAA ATGGACGTAG TCCTCTTAAT	780
TTGGAGCAGT GGCGTCTTG GATTGCCTAT GTACCTCAAA AGGTCAAACCT CTTAAGGGAA	840
ACTATTCGTT CCAACTTGAC TTTAGGTTA AATCAAGAAG TATCTGACCA GAAACTCTGG	900
CAGGGCTTGG AGATTGCGCA AGCTAAGGAT TTGTCAGTG AAAAGGAAGG ACTTTGGAT	960
GCCCTAATMG AAGCAGGGGG GCGAAATTTC TCAGGTGGAC AAAACAAAG GTTGTCTATC	1020
GCCCGAGCAG TCTTGCGCCA AGCTCCGTT ATCATCCTAG ATGATGCAAC CTCGGCACTG	1080
GATACCATTA CAGAGTCCAA GCTCTTGAAA GCTATTAGAG AAAATTITCC AAACACGAGC	1140
TTAATTTTGA TCTCTCAACG AACCTCAACT TTACAGATGG CGGACCAAGAT TCTCCTTTG	1200
GAAAAAGGTG AGTTGCTAGC TGTTGGCAAG CACGATGACT TGATGAAATC CAGCCAAGTC	1260
TATCGTAAA TCAATGCATC CCAACATGGA AAGGAGGACT AGAATGAAAC GACAAACTGT	1320
AAACCCAGACG CTCAAACGTT TAGCCGTAGA TTTAGCAAAC CATCCCTTCC TCCTTTCCCT	1380
AGCCTTCTA GGAACATTG CCCAAGTTGG CTTATCAATT TACCTACCTA TTCTGATTGG	1440
GCAGGTCAATT GACCAAGTCC TAGTGGCTGG TTCATCACCA GT	1482

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 895 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTCTGAAGGA TCCAGAAAATG CGCTTATATA TTTTATTAAA AGACGGTCAG GTTATTGGGA	60
CTTGTACGGT TGATTATCG ACTAATACGA ATTACTCTA CGGTTTAGCA ATATTGGAAC	120
CTGAACGTGG AAAAGGCTAT GGAAGCTACT TAGCAAATC CCTCGTCAAC CAACTAATTG	180
AGCAAAATGA CAAGGAATTG CAGATTGCAG TGGAAAGATAG CAATGTAGGT GCCAAACGTT	240
TGTATGAAAA AATTGGCTTT GTCAACACAGA CTCAGGTGGT TTATCTGAAT GAGAAAGGAG	300
CAAGGGATTC CGAAGTGTAG AGATATTCCG ACTGAAATTG ACTTGAACCTT TTAGTGATGA	360
AACTAATTGT TCTTGGATTT CAGCTTCCT GATTATGATT TATGATTAAA ATCTATGACA	420
CCATGTCTCG TGATTGCGA GAATTGTCC CGATTGAGGA CGGCCAGATC AAGATGTATG	480
TTTGTGGGCC AACGGTGTAC AACTATATCC ACGTGGGAAA CGCCCGTTCG ACGGTAGCTT	540
TTTTGGATAC GAATTTCGTC GCTATTTGA GTACCGTGGG TATAAGGTTG CCTATATTTC	600
CAATTTACA GATGTGGATG ATAAGATTAT CAACCGTGCC AGGGAAAGAAG GCATCACGCC	660
TCAGGAGGTT GCGGATAAGT ACATCGCTGC CTTTCGTGAG GATGTGACGG CCTTGGGCGT	720
GAAACCTGCG ACTCGCCATC CGCGTGTAGT GGAGTTTATG GCAGACATCA TCCGTTTGT	780
GGAAAGACTTG ATCGAGAAAAG GCTTTGCCTA TGAGAGTCAA GGGGATGTCT ATTTCCGTGT	840
AGAAAAATCC CACAACATATG CTAAATTGGC TAATAAAACC TTGGAAGATT TGGAG	895

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 709 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTGTTTGCCTTCTAA TAAAGAATTG GCAGAACGTG TGGCGCAGGA GATTGGGATA	60
GAGTTGGGAA AATCAAGTGT TCGCCAATTTC TCAGATGGAG AGATTCAGGT CAACATTGAA	120
GAATCAATCC GTGGGAAACA CGTCTTTATC CTACAATCAA CTAGTTGCC TGTAAATGAC	180
AATCTGCTTG AAATTTGAT TATGGTAGAT GCTTGAAGC GTGCGAGTGC AGAATCTGTC	240
AATGTTGTCA TGCCTTACTA TGGGTATGCA CGTCAGGATA GAAAGGCGAG AGCGCGTGAG	300
CCAATCACTT CAAAACCTGT CGCAAATATG CTTGAAGTAG CTGGAGTGGA TCGTTTATTG	360
ACCATCGACT TGCATGCTGC GCAAATTCAA GGATTCTTG ATATCCCTGT GGATCATTTG	420
ATGGGTGCTC CTCTGATTGC AGATTATTTT GAGCGTCCCTG GTATGGTTGG TTCTGACTAT	480
GTGGTTGTCA GCCCGGACCA TGGAGGGGTG ACTCGTGTGCTC GTAAGTTGGC AGAATTGTTG	540
AAAACATCTA TCGCTATTAT TGAGAAACGT CGTAGCGTTG ATAAGATGAA TACTAGTGAA	600
GTTATGAACA CCATCGGTAA GGTTGAAGCC AACCACTTGT AGCTTCGATT GATGATATGT	660
ATTGATAACCG CTGGAACGAT TTGTCATGCG GCAGATGCTC TTGCGGAAG	709

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CTAGAAGAAC TCCGTCACAA GCTTGTGACT TGTAAGCAAG AACAGAGCAA GATTGAGGAT	60
TCCTTATGAT TTCATTCCTT CTTCTATTGG TCTTGGTTTG GGGATTTAT ATCGGCTATC	120
GGAGAGGCCT GCTCTTACAG GTTTATTACC TGATTTACGC CATGGCATCG GCTTTATGG	180
CTGGCCAGTT TTATAAGGGG CTTGGAGAGC AATTCCATTT ATTGCTCCCT TATGCAAATT	240
CGCAGGAAGG TCAGGGGACT TTCTTTTCC CATCGGATCA ACTCTTCAG CTGGATAAGG	300
TCTTTATGC AGGTATCGGC TACTTGCTTG TATTTGGGAT TGTCTATAGC ATTGGTCGTT	360
TGCTTGGTCT TCTCTTACAC TTGATTCCTA GCAAAAAACT GGGTGGTAAG TTGTTCCAAG	420
TTTCAGCAGG TATCTTGTCG ATGTTGGTGA CCTTATTGTT CTTGCAAATG GCCTTGACAA	480
TCTTGGCGAC CATCCCCATG GCAGTTATAC AAAATCCCT TGAAAAGAGT ATCGTCGCAA	540
AACACATCAT CCAGAGCATA CCGATAACAA CCAGTTGGCT CAAACAAATC TGGGTGACAA	600
ATTTAATCGG ATAAAAAGGG CAGGAGTTT CCTAGCCCTT TGTTTACAGA TTTGACTCGA	660
ATCTATCAGA ATGTAAAAAG CTACCACACC TAGACATTCA AAGACAAGGA AATAAAGATG	720
AATAAGAAA TATTAGAAC ATTAGAGTTC GATAAGGTCA AGGCCTTGTG TGAGCCTCAT	780
TTGTTGACCG AGCAGGGCTT GGAGCAATTG AGACAG	816

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 1001 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTTGAAGCAG CTGAAAGCAT GGGGTCTTCG GGATTTAAAA CCTATTCGTA ACGGGTTGTT	60
TTACCTTCC TAGTCCAAC CTTACTAGCA GCTCCTTGCT TGTATTTATG AGAGCATTCT	120
CAGACTTGG AACGCCATG TTGATTGGCG AAGGATATCG GACTTTCCCT GTCTGATTT	180
ATACCCAATT TATTAGCGAG GTTGAGGAA ATTCTGCTTT TGCAATTATG GCGATTATCA	240
TTGCCTTGGC AATTTTCCCT ATCCAAAAAC ACATTGCAA CCGCTACAGT TTCAGCATGA	300
ATCTGCTCCA TCCAATTGAG CCTAAAAAAA CTACAAAAGG AAAAATGGCT GCCATTTATG	360
CAACAGTCTA CGGAATTATC TTATCTCTG TTTTACCTCA AATCTACTTA ATTATACCT	420
CTTTCCTAAA AACATCAGGT ATGGTATTG TTAAAGGTAA TTCTCCAAAC AGTTACAAGG	480

TAGCTTTCAA TCGTATGGGA TCTGCTATTT TCAATACCAT TCGTATCCCT TTGATTGCCT	540
TAGTTCTAGT TGTTCTATT TACGACATTT ATCTCCTACC TAGCCGTTAG AAAACGGAAT	600
TTGTTTACAA ACTTAATTGA CAGCCTCAGT ATGGTACCTT ATATTGTACC AGGAACCGTT	660
CTAGGGATTG CCTTCATTTC TTCCCTCAAT ACTGGTCTAT TTGGAAGTGG ATTTCTTATG	720
ATTACAGGGA CTGCTTCAT CTTGATTATG TCTCTATCTG TCAGAAGAGATT ACCGTATACT	780
ATTCGCTCAT CTGTTGCTAG CTTACAACAA ATAGCACCAA GTATTGAAGA AGCTGCTGGA	840
AAGCTTAGGA AGTAGTCGTC TCAATACCTT TGCTAAGATT ACAACTCCAA TGATGCTATC	900
TGGTATCATT TCTGGAGCCA TCTTATCTTG GGTCACAAATG ATTTCAAAAC TCTCTACTTC	960
TATCCTCCCTC TACAATGTCA AAACAAGAAC AATGACTGTAG G	1001

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1064 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTGGTTTGCA ATCTATTCCA ACTGAGATTA CAGAGGCAGC AAGGATTGAT GGTGCGACTA	60
GCAAGCAAGT TTTCTGGAAC ATTGAATTGC CTTACTTGCT ACCAAGTGT C TCTATGGTCT	120
TTATCCTAGC CCTAAAAGGT GGGCTGACTG CCTTTGACCA AGTCTTGCC ATGACCCGTG	180
GTGGTCCAAA CAATGCCACA ACCTCACTTG GGCTCTTGGT TTATAACTAT GCCTTTAAAA	240
ACAACCAATT CGGTTATGCC AATGCCATTG CCGTAATCTT GTTCCCTTTA ATTGTAGTGA	300
TTTCGATCAT CCAATTGAGA GTATCTAAGA AATTGAAAT TTAAGAGGAG AACCATGATG	360
AAACAAGATG AAAGAAAAGC CCTGATTGGC AAATACATTC TATTGATTCT AGGATCGGTT	420
CTGATTTAG TGCCGCTCCT TGCTACCCCTC TTTAGTTCTT TTAAACCCAC TAAGGATATT	480
GTAGATAATT TCTTTGGCTT TCCAACCAAC TTCACATGGG ACAACTPTAG CCGTCTCTTA	540
GCTGATGGGA TTGGAGGCTA TTATTGGACT CTGTCGTAT CACTGCTTG TCTTTACTTG	600
CAGTAATGAT CTTTATCCCT ATGGCAGCCT ACTCCATCGC TCGCAATATG AGTAAAAGAA	660
AAGCCTTAC CATTATGTA TACCCCTTTA ATCCCTGGAA TCTTCGTACC TTTCCAAGTC	720
ATCATGATTC CGATTACGGT TATGATGAGT AAACCTCGTT TGGCTAAATAC CTTTGGTTTG	780
ATCTTGCTCT ACTTGACCTA TGGGATTCCA CAGACCCCTCT TTCTCTATGT TGGATATATC	840
AAAATCTGA TTCCAGAAAG TCTGGATGAA GCAGCAGAGA TCGATGGGGC TAATCAATT	900
ACAACCTATT TCCGCATCAT NTTCCCAATG ATGAAACCGA TGCATGCGAC AACCATGATC	960
ATCAATGCC CTTGGTTCTG GAATGACTTC ATGTTGCCAC TCCTTGTCTT GAACCGGGAT	1020
TCCAAAATGT GGACTCTGCC TTTGTTCCAA TACAACCTACG CAGG	1064

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTGTAAAAGA AGTTAACAA GTTGATAAAG CACTTTAAA ACAAAATTGGT GCAGTTGATG	60
TCTTAGAAGT GAAGGGTGGC ATTCAAGCAA TCTATGGAGC AAAAGCAATC TTATATAAAA	120
ATAGTATTAA TGAAATTGTTA GGTGTAGATG ATTAAGTACT TACTGACTTA ATAAAAAAACA	180
GAGGAGAGTG ATGGATGAGT AGGATGAAAT GAAATCGCAT ACAAGAAATA AAGAACTCAT	240
TATCCAAGTT GGATACGCTT ATTACATAGG AGAATACAAA TGAAATTAGT AAAATTAGCT	300
TGTACAGTAC TTGCGGGTGC TGCAGGTTCTT GGTCTTGCTG CTTGTGGCAA TTCTGGCGGA	360
AGTAAAGATG CTGCCAAATC AGGTGGTGAC GGTGCCAAAA CAGAAATCAC TTGGTGGGCA	420
TTCCCAGTAT TTACCCAAGA AAAAAGCTGGT GACGGTGGTGA GAACTTATGA AAAATCAATC	480
ATCCAAGCGT TTTGAAAAAG CAACCCAGAT ATAAAAGTGA ATTGGAAAC CATCCACTTC	540
CAGTCCAGTC CTGAAAAATC ACAACAGCCA TCCGAAGCAG GAACAG	586

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TGGTAGTTCT TCCTAGTGCA GGGGCTGTAG ACCCAGTTGC GACCCTAGCG CTGGACTAGT	60
CGAGAGGGTG TTGTTGAAAA TGGATGGNTA TCGCTATGTT GGTTATCTAT CAGGTGACAT	120
CCTCAAAACG CTTGGCTTGG ACAGTGTGTT AGAAGAAACC TCAGCAAAAC CTGGAGAGGT	180
GACTGTAGTC GAAGTTGAGA CTCCTCAATC AACAAACAAAT CAGGAGCAAG CTAGGACAGA	240
AAACCAAGTA GTAGAGACAG AGGAAGCTCC AAAGAAGAAA GCACCTAAA CAGAAGAAAG	300
TCCAAAGGAA GAACCAAAAT CGGAGGTAAA ACCTACTGAC GACACCCTTC CTAAGTAGA	360
AGAGGGAAA GAAGATTCA CAGAACCATC TCCAGTTGAA GAAGTAGGTG GAGAAGTTGA	420
GTCAAACCA GAGGAAAAAG TAGCAGTTA GCCAGAAAGT CAACCATCAG ACAAAACCAGC	480
TGAGGAATCA AAAGTTGAAC CACCAAGTAGA ACAAGCAAAA GTCCCAGAAC AACCCGTGCA	540
ACCTACACAA GCTGAGCAAC CAAGTACACC AAAAGAATCA TCACAAACAAG AAAATCCTAA	600
AGAAGATAGG GGAGCGGAAG AGACACCGAA ACAAGAAGAT GAACAGCCAG CAGAAGCCCC	660
AAGAAATCAA GGTTGAAGAA CCAGTAGAAT CAAAAGAGGA GACTGTTAAT CAACCTGTTG	720

AACAACCAAA	AGTGGAAACG	CCTGCTGTAG	AAAAACAAAC	GGAACCAACA	GAGGAACCAA	780
AAGTTGAAGT	AACAAGTATT	CCCCAAACTA	CTCGCTATGA	GGAAGACCTT	ACTAAGGAAC	840
ACGGAACGCG	TGAAGTTGTT	AAGGAAGGTA	AGAATGGCAG	TAGAACAGTT	ACTACTCCAT	900
ATATCTTGAA	TGCGACAGAT	GGTACGACTA	CAGAAGGCAC	TTCGACAAC	GATGAAGCTG	960
AGATGGAGAA	AGAGGTTGTT	CGTGTGGCA	CGAAACCCAA	AGAAAAATTAA	GCTCCAGTCT	1020
TAAGTTTGAC	AAAGTGTACAA	GATAATGCAA	TGTTGCGTAG	TGCGAGACTT	ACTTATCATT	1080
TGGAAAATAC	AGATAGTGT	GATGTGAAAA	AAATTCA	TGAAATTAAA	AATGGCGATA	1140
AGGTTGTCAA	AACTATTGAC	TTATCTAAAG	AGAGATTATC	AGATGCTGTT	GACGGTCTTG	1200
AACTTTATAA	AGATTATAAG	ATTGTGACGA	GTATGACCTA	TGATAGAGGT	AATGGTGAAAG	1260
AAACCTCTAC	GTTGGAAGAA	ACTCCACTAC	GATTAGACCT	CAAGAAGGTT	GAATTGAAAA	1320
ACATCGGCTC	TACTAATCTC	GTCAAAGTAA	ATGAGGATGG	TACTGAGGTG	GCAAGTGACT	1380
TCTTAACAAG	AAAACCTGTG	GATGTGCAGA	ATTACTACCT	CAAAGTAAC	TCCC GTGATA	1440
ATAAAAGTTGT	TTCCCCCTCCC	AGTTGAAAAA	ATTGAAGAGG	TGACTGAGGA	AGGTCCACCA	1500
CTTTACAAAG	TCCCTGCTAA	GGCCCTAATT	TGAT			1534

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGGATTGTT	TATCTCAAGA	AGAGTCGCGA	TATTCTCCGT	GAAAGTTCA	AATTGATTAN	60
CCAAACGGTA	GAAGATTATC	TTCAAGGAGA	TGACTTTGAC	TGGGCAGATC	TTAAAGGGAA	120
GGTTCGANAT	AATTGACCA	AGTATCTCTT	TGACCAAACC	AAGCGTCGTC	CANCTATT	180
ACCAAGTAGTC	ATGGAAGCAA	AATAATCGTT	GAAATAAAC	GAGAGAAAGT	CGAGTTTCGG	240
CTTTTTCTTA	TAGAAAAATA	GAAGGAGAAA	ATCATGGCAG	TAATGAAAAT	CGAGTATTAC	300
TCACAAGTAT	TGGATATGGA	GTGGGGGGTG	AATGTCCTCT	ACCTGTATGC	CAATCGAGTG	360
GAAGAACCAAG	AGTGTGAAGA	TATTCGGCTC	TTGTACCTT	TGCACGGGAT	GTCTGGAAAT	420
CATAATAGTT	GGCTTAAGCG	GACCAATGTA	GAACGCTTGC	TTCGAGGAAC	TAATCTCATC	480
GTTGTTATGC	CCAATACCAAG	CAATGGTTGG	TACACCGACA	CCCAGTATGG	TTTGACTAC	540
TACACGGCTC	TAGCAGAGGA	ATTGCCACAG	GTTCTGAAA	CGCTTCTTCC	CTAATATGAC	600
TAGCAAGCGT	AAAAAGACCT	TTATCGCTGG	TCTTTCTATG	GGAGGCTACG	GCTGCTTCAA	660
ACTGGCTCTT	ACGACAAATC	GT	TCTCA	TGCAG		695

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1096 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CTCATCCAAG AATAGCATAA AAGAACTCTT CTGTTTTTC TTGAGGAACG AGAAAGTCAG	60
CAATCTCCAT TCCACGATCC ATCAAATCCT CTAAGACAT CGTGATTTT AAAGTAGTAT	120
CACTAATTG TTTCATTTTC ATTGCTAGTA ACCTCATACT TTCAGTTCTA TCTATTATAC	180
TAGATTTTTA CGATTTTATC AAAAGAAGGC TCCTCTATAC GGATAGATTT TCCCTAGGGT	240
CTTTCTATAG GAGACTCCAA GAGAAAATTT CTGCAGACAG ATAGAAAAAG CCTTCAAAAT	300
CGGCTCTTAG CCGATTTGA AGACCTTATA CATCAGAATA CTTATAATTT AAAGGTTGCT	360
ACACCGAGGA TAGAACGATT TAAGTTCTG AGAATTGAA GACTTTGCTC AAATTCTTA	420
TAACGAATTC ACTCCGTACT CTTCAACAAG AAGGACTGTA TCTCTTCCA AAAGAGATGA	480
TACATCCTGC AAATCTACAA ATGCATTCCCT TTTAAAGCTT CTTGACTCTG TTTCAATTAA	540
TCTAGGATAG CTTTATTGTA GCTAACGATG GTCAATTCTC GTCCAGTATT TTTGATGAC	600
AAAACATCTG CTAGGTTAGC AATTGTTGTA ATCTCTGTTA CAAAATCAAT TTGATACTGA	660
GAAAATCAC CTACTCTATT GATTGTTGGA TAAAGAGAT AACTAACAC ATTTCCCAC	720
ACAACCAAAA TCACACAAAC CACTCCAATA ACAACTAAAC GAAGAACAG ATTTTCACA	780
TTTAAGCCAA GCGCTGTTTC ACCATTGCG TTCAATTCTT TAGAGTTGAT GGTTCAGT	840
TTTTCAATTTC TCACATTGTC ATAAGCATGT TTAAATTCT CAATCAACCC ATCAATTTC	900
TTCTCTAACCA AGTCATTGGC ATCTTACTT GATGTCAAAA TTTTCACACC AACCCCTGCA	960
TCGTCAATCA TATAGTAGAC GGTCAATTTC TTCCACCAAT AGTCATTGCT TGAATTTC	1020
AAGGTTGTTT CCGTCGTGTC TAATTCACTG GCAATTTC TCAACTCACT GGGTTCTACA	1080
TCATTGAAAAA GATAAG	1096

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1037 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TCCCCATCCC AGTGGGCAGC AGCATTAGTC TGACTTCTG CGTCGTTGCG TTTTATTAGA	60
AGACTGATTG TGCTTTGAAC TACTTGAAGC TGTCGTTGTA TCCTGCGAAG TTTTTGCTAA	120
CTTCAGTTTC ATTTGCAGCG ACATGACTAG TTGCCAAGCC TAGTAAACAG ATACTTGCTA	180
ATCCAATTTC TGTGTTCAAT CTTTCCTCTC CTATAAAAAA TGTAACAGAC ATCTGAATGC	240

TGTTCCACCT AGCTTTGCT ACTTACTGAT TATTTACAA AGTCAGCAA AGCCAAGAAG	300
CTTTCAGCTT CAAGTGACGC ACCACCTACA AGGGCACCGT CAACGTCTGG GCAAGCCATG	360
TATGAAGCAA CATTTCAGG TTAAACAGAA CCACCGTATT GAACACGAAC TTTGTCTGCC	420
ACTTCTTGAC CAAAGTCAGC AGCTACAACG TCACGAACAA CTTCACACAT TTTTGTCGCA	480
TCGTCTTG TG AAGCTGATT ACCAGTACCG ATAGCCCAGA TTGGCTCATA AGCGATAACT	540
GAGGCAGCAA CTTGTTTCAGC AGTCATAACCA GCCAATGCAG CAGATACTTG AGCACCTACG	600
AATTTCAGCAG CTTTACCAAGC TTCGTAAGTT TCAAGTGATT CACCACAAACA GATGATTGGA	660
AGCATACCGT TCGCAAAGAT TGCTTTTGCT TTTTGTTGA TATCTTCGTC AGTTTCATGG	720
AAGTAGTCAC GGCCTTCTG AGTGACCGAT AACAAACGTAG TCAGTACCGA TTTCTTCAA	780
AACTTGTGGG CTAGTTTCAC CAGTGAAGAC ACCTGCATT TCTCCGTAGC AGTTTTGAGC	840
AGCGACTTTT AAGTTTGAGC CTTNGCAAC AGCAAGNACA GTTGTCAAAT CAAGAGCTGG	900
AGCAGNGATA CCTGCTTCAA CAAGATCTGA TGAAGGAAGT TTTGATGCAA CTGCTTCAC	960
GAATGNTCCA GCTTNTTGGG GATTTTGTT CATTTCAG TTACCAAGCGA TAAATGGTTT	1020
ACGTGACATT TCACATA	1037

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CTTATCGTAC TAAGGATGGC AGTGTCAAC TGTTCCGTC TGATGAAAAT GCTAAACGCC	60
TGCAACGTAC ATGTGACCGT CTCTTGATGC CAACAAGTTC CGAACAGACA TGTTTGTAGA	120
AGCTTGAAA GCAGTTGTCC GTGCGAATGA AGAATACGTA CCACCATACG GAATAGGTGG	180
AACTTTATAT CTTCGCCCTC TTTTGATIGG TGTCGGAGAT ATTATCGGGG TAAAACCGGC	240
AGAAGAGTAC ATTTTCACCA TCTTTGCTAT GCCAGTTGGA AATTACTTTA AAGGTGGTTT	300
GGTCCCACCC AACTCTTGA TTCAAGGATGA GTACGACCGT GCAGCACCAA ATGGTACAGG	360
TGCGGCTAAG GTTGGTGGAA ACTATGCTGC AAGTCTCTTA CCAGGAAAAA TGGCCAAGTC	420
ACGCCATTTC TCAGATGTTA TCTATCTGGA CCCATCACT CATAACAAAGA TTGAAGAAGT	480
CGGATCAGCT AATTCTTTG GAATTACAGC TGATAATGAA TTTGTAACAC CATTGAGTCC	540
ATCTATCTG CCATCTATTA CCAAGTATTIC CTTGCTTTAT TTGGCAGAAC ATCGCTTGGG	600
ATTAACCTCT ATTGAGGGTG ATGTTCCAAT TGATAATCTT GACCGTTTG TAAAGGCAGG	660
TGCCCTGTGGT ACAGCAGCGG TTATTTCTCC AATTGGAGGT ATTCAACATG GTGATGATT	720
CCATGTTATT CTATAGTGA ACAGAAGTAG GTCCTGTGAC ACGTAAATT AATAATGAAT	780
TGACGGGTAT TCAGTTGGC GATATTGAAG CCCCGAAGG TTGGATTGTA AAAGTAGATT	840
AAAATAAACC AAAGGAGATT TTTTATGAAA TAGAAAAAGT GCCTCTTAAC AGCAGGAGTG	900
GTCCTGAGCA CGTCAGCTAT TTTAGTGGCT TGTGGAAAAA CTGATAAAGA AGCAGATGCA	960
CCGACAAACAT TTTCTTATGT CTATGCGATA GATCCAGCAT CATTGGGCTA CAGTATAGCG	1020

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ACTCGAACAT CGAGGACAGA CGTTATTGGA AATGTTATTG ATGGTTTGAT GGAAAATGAT	1080
AAATAACGGCA ATGTTGCTCC TTCTCAAAAA GACTATGATT TGAACAGTAC AGGATGGGCT	1140
CCAAGCTATC AAGATCCAGC GTCTTACTTG AATATTATGG ATCCAAAATC TGGTTCTGCC	1200
ATGAAACACC TTGGCATTAC GAAAGGAAAA GATAAGGATG TTTGTAAC TAACCTGGTTT	1260
GGATAAAATAT AAGAAATTGT TAGAAGATGC TGTTTCTGAG ACCACTGACC TAGAGAAGAG	1320
ATATGAAAAA TATGCCAAAG	1340

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CTCTGACGGC GTCGCCACTT AAGAAGAGTA TCaaaaAGAA AAATAGAAAA TTAACAAACA	60
AGGNAGAAAA ACACATGTCT AAAATTATCG GTATTGACTT AGGTACAACA AACTCAGCAG	120
TTGCAGTTCT TGAAGGAACT GAAAGCAAAA TCATCGAAA CCCAGAAGGA AACCGCACAA	180
CTCCCATCTGT AGTCTCATTC AAAAACGGAG AAATTATCGT TGGTGATGCT GCAAAACGTC	240
AAGCAGTCAC AAACCCAGAT ACAGTTATCT CTATCAAATC TAAGATGGGA ACTMTCTGAAA	300
AAGTTTCTGC AAATGGAAAA GAATACACTC CACAAGAAAT CTCAGCTATG ATCCCTCAAT	360
ACTTGAAAGG CTACGCTGAA GACTACCTTG GTGAGAAAGT AACCAAAGCT GTTATCACAG	420
TTCCGGCTTA CTTCAACGAC GCTCAACGTC AAGCAACAAA AGACGCTGGT AAAATTGCTG	480
GTCTTGAAGT ANGACGTATT GTTAACGAAC CAACTGCAGC AGCTCTTGCT TATGGTTTG	540
ACAAGACTGA CAAAGAAGAA AAAATCTTGG TATTTGACCT TGGTGGTGGT ACATTCGACG	600
TCTCTATCCT TGAATTGGGT GACGGTGTCT TCGACGTATT GTCAACTGCA GGGGACAACA	660
AACTTGGTGG TGACGACTTT GACCAAAAAA TCATTGACCA CTTGGTAGCA GAATTCAAGA	720
AAGAAAACGG TATTCGACTT GTCTACTGAC AAGATGGCAA TGCAACCTTT GAAAGATGCG	780
GCTGAAAAG CCAAGAAAGA CCTTTCTGGT GTAACTTCAA CACAAATCAG	830

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GTGGTGGTTT	GAUTGCCCTT	ATCGAAGCAG	GTTTCGAANT	CTAACACANA	AGCAGGTTAC	60
GCTCCAGAAT	TGGCTTAACT	TTGAAGTTCT	TCACGGAAAT	GAAATTGATC	GTTGACTTGA	120
TCTACGAAGG	TGGATTCAAG	AAAATGCGTC	AATCTATTTC	AAACACTGCT	GAATACGGTG	180
ACTATGTATC	AGGTCCACGT	GTAATCACTG	AAACAAGTTAA	AGAAAATATG	AAGGCTGTCT	240
TGGCAGACAT	CCAAAATGGT	AAATTTGCAA	ATGACTTTGT	AAATGACTAT	AAAGCTGGAC	300
GTCCAAAATT	GAUTCCTTAC	CGTGAACAAG	CAGCTAACCT	TGAAATTGAA	AAAGTTGGTG	360
CAGAATTGCG	TAAGGCAATG	CCATTGTTG	GTAAAAACGA	CGATGATGCA	TTCAAAATCT	420
ATAACTAATT	AGAAAATATAT	AGCGCTGGAG	ATGATTTTAT	GAAAAGATT	ATGAGAAAAA	480
TTGCATCGTT	ATTATTTGGTT	CTAGTTGTAT	AATGTAATTAA	CACCGTCGGT	AATAGTGCTA	540
GCAGACCAAA	ATAAAGCAGA	TTGGTCGTAT	GATGAAAATA	CTGTAATTAA	CATTTATGAT	600
GATGCTAATT	TTGAAGATGG	TAGGTTGCAT	ATGACCTTIG	AACAATTCTT	CAAATTGGCA	660
CAAATAG						667

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CGGTTCCAGA	NACTGGTATG	GCTAGGAGTC	GCGACAAAGT	GTATCTTATG	ATGGTCGATT	60
TGATACTCAA	TACGCTCAAT	ACTTACGGAA	AGAATAAACG	ATCATTGTCA	ACCGGAATAG	120
TATGATAATC	GTTCCTTGGT	GGAATAAGTT	CAATCTTATC	CTTCTTAGGC	ACAATAATGG	180
AAGAGCCCAG	TGTTCGATAA	ACACGATTAT	TAAGGCTGGC	AATTTCGGTT	AATTGCAAAC	240
CTTCAATGGT	AGGGTGTAAA	ACAGCACCCAC	CAAGAGACTA	GTTATAGGCA	GTACTACCAG	300
TCGGTGTGCA	AACTGTTAGC	CCGTCTCCAC	GAAAACGTTTC	AAAGGGAAACA	CCATTTATTA	360
CAATATCTGC	CACCATGGTT	CGATCAGACC	TGCGGATGCT	GGCTTCGTTG	AGTGCTCTGA	420
AAATCTTAAC	TTCACCATT	TCAAGAAAGA	CCTTCACATT	CAGAACAGGG	TAAGAAACCC	480
TTGCCCCAGT	ATCTAGCTGC	AAATTAGTCA	CTAGCTTGTCA	CAACTCAAAA	TCACGATAAT	540
CTGTATAGAA	GCCCAAATGT	CCAGTATGAA	GACCGATAAA	GCGGACCTTG	TCAAGCTGAT	600
TTTCGTACTT	ATGAAAGGCC	GACAAGAGCA	TACCATCCCC	GCCAATGGAA	ATGACAATAT	660
CCGGATTGGT	ATCATTGAGT	TATAAACTGA	TTTCTCTTCA	AACGATCTCG	CAATTCTAC	720
AAAACCCATT	GACTCTGCAGG	TTTTCTATTG	GCTATCAGAT	CAATTGTTT	ACCTGTATTG	780
TTTCATCTGTA	TCGTCACTGN	NTCCAACACC	GTCATTTAAT	TTTCTACTCA	AAGGATCAA	840
AAGTGCCTGG	GCTTCCTTGGG	TATCATCACG	AATTTCACCC	ATTTCTTCAT	CCAACGTGATG	900
GGCGATTCTA	GCTGTAATT	CCAGTCGCTT	CTTAATCTCA	TCTGGAAAT	CCCCTTGGTA	960
CTTGTAGTTG	AGAGAATGTT	CTATCGTTGC	CCAGAAATTG	ATGGCCAAAG	TACGAATTG	1020

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AATTTCTGCC	AAAATAGTCT	TAGCTCCATT	GATGGTATCA	ACCGTATATT	CTACTACCAC	1080
ATGATAGGAA	CGATAGCCTG	ATGCTTTCT	ATGAGTAATG	TAATCTCGCT	CCTGTATGAT	1140
TCGCATATCC	TGACGCTGT	GCAAATATC	CACTACTTCC	TTGACGTCAT	CTACAAACTG	1200
AACCATCACA	CGTAAGCCAG	CAATATCCTG	CAAATCGTGT	TCCAAGGTCG	CATAAGTAAT	1260
GCCACGACGA	GCCATTTTT	CTTGATGCT	CTCAATTGGC	TTGACTCGAC	CGGTACACAAA	1320
CTCAATTGGA	GAATGTTAT	TTTGCTTACG	ATATTGCTTA	CGAATACAC	GAAGTTTAAT	1380
CTTTAACTCA	CCAACAG					1397

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CTCCCCATGAC	ACCTGCACGC	TCCGTACGGG	CCACGTGCTT	TTTAATCCGT	TCAACAACTT	60
CATAACCCGC	TTCAACATCC	ACACCCGACT	GGGCATATGC	ATTTTATTT	GTCATTGTT	120
TTTTCCCTTT	CTTTAATGGA	GAATCTGTCG	CCTACTTGTA	AAAACTGGTC	TTTTCTTCCA	180
AACTTCTACG	ATAGTCTTCT	TCGTAGTCAT	AGAGAGGCGT	TGGTAGTCA	CCGTCAAAGT	240
AAGCGACACA	GAGACCACCG	TTCGGCGCAT	CTGTTTCGAT	ACCAATCGAC	TCAATCAAGC	300
TATCAATTGA	AAGATAAGTC	AGACTGTCCG	CACCAATGAT	TTGGCGAGTT	TCTTCGACCG	360
TATGATTGGC	TGCAATCAGC	TCCGTACGGG	TCTGGATATC	AATCCCGTAG	AAACATGGAT	420
ACGCTAGTGC	AGGACTTCCA	ATGGCAACGT	GAACCTCAGT	CGCACCCGCT	TCTTTCAAGA	480
GCTGAACGAT	ACGACGAGAG	GTTGTTCCAC	GTACAATGGA	ATCATCCACC	ATGACCACAC	540
GTTTGCCTTT	GACAACACCC	GAAACAGCAG	ACAGTTCAT	CCGCACTCCT	TGCTCCCGCA	600
ATTCTTGAGT	CGGTTGGATA	AAAGTTCGCT	GGGTGTATTG	GTTTTGATC	AGACCCATT	660
CATTTGGTAA	CCCTGATTCT	TCCGCAAATC	CCATAGCCGC	GCTTAGGGAA	GAATTGGGCA	720
CACCAACTAC	AATATCTGCC	TCATGCTTAA	ATTCTCGCGC	CAATTGCGCT	CCCATTCTCT	780
TACGTGCCGT	ATGGACATTG	ACCCGTGGAT	ATTAGAACATCA	GGGC		824

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTTCTTCCTT	GGTACTTCCT	CAATTGGATT	ACCTTTGGCA	TTGCTAGTTT	TTCACTCCTA	60
CCTTATATCC	AAGGCACTAA	AATTATGTTT	TACCGAGCAG	TATTGGCTCG	AAAACGTCCA	120
AAAGCTGAA	GGTTTCCCC	TCAAGCTTT	TTCTATCAAT	GAATTCTCC	GCCTACCAAC	180
GTGAGTTCC	GATCTCCATG	TTCTATCAT	GCGCCGATTG	CTGCTTCTAT	CCCTCGCCGA	240
ATATCCACTA	AACTCATAGT	TGGAGTAGTC	GGTCTGTTCA	CCACCTGTC	CATCATATAA	300
GGAATATGCA	TAAAACCTGC	CTTAACATAT	GGGAATTCT	TTTCTACCAA	ATAGAGAGCC	360
TGATACATCA	AATGACTGCA	AACAAAAGTC	CCTGCACGTA	TTGGAAACAG	ACTGCCGGTA	420
AGTCCTTC	TTTATTAGC	TTGTACCATC	GCTTTGATAG	GTAAACTACT	AAAATAGGCC	480
GATGCTCCAT	CAATACGAAT	CGGTGTATCA	ATTGGTTGAT	TGCCTTCGTT	ATCAGGTATG	540
CGAGCATCAT	CTTGATTAAT	AGCCACTCGT	TCAGGTGTTA	AGCCGGCTCCT	GCCGCCCTGCT	600
TGTCCAATAC	AAAGTACAGC	ATCTGGTTGA	TATCGTAATA	TTTCTGCCTC	AAAAACTTCT	660
GACGACTTAT	AAAAAACCGT	TGGAATTCT	ACCCAGCGAA	CTTCAGCCCC	ATTAATCTCA	720
GATGGTAATA	ATTTTACAGC	CTCCAAAGCT	GGATTAATCT	TTTCACCTCC	AAAAGGATTA	780
AAACCTGTAA	CCAATATTTT	CATTTTATTT	TCCTTTACTA	AAATGCGAGA	AAGTACATTA	840
AGAATATGTG	AATAACAATC	ATTACTAGAG	CAACACCTGC	TTGAGCCTTT	ATAACGCCAT	900
TCTGATCTT	CATATCCATC	AATGCTGCTG	GTAGAGCGTT	AAAATTAGCA	GCCATTGGGG	960
TCAATAAGGT	CCCACAATAA	CCTGCTGTCA	TGGCAAGAGC	ACCAGCCACA	ATTGGATTAG	1020

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTCGTAAAAA	CACTAAAGGA	GGTAAATAAC	CAATGTTAGT	ACCTAACGT	GTTAACACACC	60
GTCGTGAATT	CCGTGAAAAA	ATGCGCGGTG	AAGCAAAAGG	TGGAAAAGAA	GTAGCATTCG	120
GTGAATACGG	TCTTCAAGCT	ACAACTAGCC	ACTGGATCAC	TAACCGCCAA	ATCGAAGCTG	180
CTCGTATCGC	CATGACTCGT	TACATGAAAC	GTGGTGGTAA	AGTTTGGATT	AAAATCTTCC	240
CACACAAATC	ATACACTGCT	AAAGCTATCG	GTGTGCGTAT	GGGATCTGGT	AAAGGGGCAC	300
CTGAAGGTG	GGTAGCACCA	GTAAACGTG	GTAAAGTGT	GTTCGAAATC	GCTGGTGTAT	360
CTGAAGAGAT	TGCACGTGAA	GGCCTTCGAC	TTGCTAGCCA	CAAATGCCA	GTAAATGTT	420
AAATTCTGTA	AACGTGAAGC	AGAATAAGGA	GAAGGCATGA	AACTTAATGA	AGTAAAAGAA	480
TTTGTAAAG	AACTTCGTGG	TCTTCTCAA	GAAGAACTCG	CGAAGCGCGA	AAACGAATTG	540
AAAAAAGAAT	TGTTGAACT	TCGTTCCAA	CCTGCTACTG	GTCCAATTGG	AAACAAACAG	600

WO 97/37026

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTTCAGCGAC ATATCTATCC ACAACTTCTC TCGATTCATG TTCCCTTGAA AATGCCGTGAA	60
ATTTTAATTG ACTAATTGAA TCCTGATACG AACTATCTGC TAACAAAAACT TCAAGATGGG	120
AAACATTTGC TAACGGATAA GGTCTTCTAT CCTTACCTAA CCAAGTTCT GTCTCTTCAT	180
CCTCTATTAG TCCCCAGTTA CTGGCAAAGT CAGGATGATT CTCTAAAAAA ATACGTTCTG	240
TCTGAAAAGT GACTGACCGA ATGGGGAAAG AAGCTGTTC TCTCTCAAAA CTAGTAAACA	300
ATGCACGCCA AATCCCCTGA CGGCGATGAC CTGGATGAAC CAGTATCGTC ACTTCTACAT	360
CTTGGTCATC TGCATAGACA GTTAATAAAC CAACAAGTTC GCCTTTTCA TAATAAAGGA	420
AAAAGGCGGG CATGTTTGA TCAAAATTAA GCATGTTAGA GAGATAGGGA TCGCGATAGG	480
TACCGTCATA GTTTGGCAA CAGTTAATTAA CTTTTTCGCG CTCAGATAGC TCTTCTTGGC	540
TTAACTTGTT TCTTGCTGA ATCATATAGG TATCCTCTAC AAACCAGACG ATCTGTGACT	600
GGCATCTTTA GCCTGCTCGA GTTTATTGAC ATAATACTCC CGTTTTCTT CGACTTCGTG	660
AATAACAGGC TCATCTTCT TACCATGAAG ACGGACAATC TTGGCCGGAA TACCGACAAC	720
CGTCACATCA CTAGGTACAT CTGCTACGAC AACTGCTGCA GCACCGACCT TGGCATTTC	780
ACCAATTCC ACAGGGCCGA TAACTTGGGC ATGGGCTGAT ATGAGGGCTC CCTTTCTGTAC	840
AGTCGGATGG CGTTTGCCAC AGTCTTCCCC TGTTCCCCCG AGAGTCACTC CGTGATAGAG	900
AAGAACGCCT TTTTCAACAA TCGCTGTCTC TCCAATCACC AGACCAAGAAC CATGGTCAAT	960
AAAGACACCT GAATCAATCT GGGCTCCTGG ATGAATCTCA ATCTGAGTCC AAAAGCGCCA	1020
AAACTGACTG TGCATACGAG CTAAGAGTTT GAAGTCGTAC TTCCAGAGAA AATGCGAGAG	1080
ACGGTGGGCC GCCAAGGCCT TGACACCTGG ATAAGTCAGC AAAACCTCCA AAGTGGTGCG	1140
GGCCGCTGGA TCATTTCTT TTACGATATC AATGGTTCG CGCCACCA ACCATACATT	1200
CTCCTTTCT TACTCTGAAT CTT	1223

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGTGAGTGCC	TTTATTAGCG	GAGCPTCTCA	AGTGATTGTT	GCCTTGATTA	TCTTCCTTTC	60
ATGCTCTTTT	ATCTCTGCG	TGATGGGAAA	GGCTTGCCTA	ACTATTGAC	CCAATTCTT	120
CCAAGCAAAT	TGAAGAAC	TGTTGGACAA	GTTCTATCAG	ATGTGAATCA	ACAGTTGTCC	180
AACTATGTT	GAGGGCAAGT	GACAGTGGCT	ATTATTGTTAG	CAGTAATGTT	TATCATCTTC	240
TTCAAGATTA	TTGGTCTACG	CTATGCGGTT	ACGCTGGGGG	TTACTGCTGG	TATTTAAAT	300
CTGGTCCCTT	ATCTTGGTAG	CTTCTAGCC	ATGCTTCCTG	CCCTAGTATT	GGGTTTGATT	360
GCTGGTCCAG	TCATGTTTT	GAAAGTAGTG	ATTGTCTTTA	TTGTAGAAC	AACTATTGAA	420
GGCGTTTTTG	TCTCTCCATT	GATTTGGGA	AGTCAATTAA	ACATCCACCC	TATTAATGTT	480
CTCTTGTGTT	TGTTAACCTTC	AGGATCTATG	TTTGGTATCT	GGGGAGTTTT	ACTTGGTATT	540
CCGGTTTATG	CCTCTGCTAA	GGTTGTCATT	TCAGCCATTT	TCGAATGGTA	TAAGGTAGTC	600
AGTGGTCTAT	ATGAATTAGA	GGGTGAGGAA	GTCAAGAGTG	AACAATAGTC	AACAGATGTT	660
ACAGGCTTTG	GAGGACCAAG	ATTTAACTAA	GGCTGAGCAT	TATTCGCCA	AAGCTTTAGA	720
AAATGATTCA	AGTGATCTTC	TGTATGAGTT	GGCAACTTAT	CTTGAAGGGA	TTGGTTCTA	780
TCCTCAGGCC	AAGGAAATT	ACCTGAAAT	TGTAGAACAT	TTTCCAGAGG	TTCATCTTAA	840
TCTAG						845

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CTATGGATTA	ATCTTCTTCT	ATCTTATCCT	GTTCTAAAT	ATGTTGGTAG	AAAAATGAAG	60
CAGTTGTTAC	GAGTGTCTGT	ATTGGAAAAA	AATTTGTCT	ATACAATTCT	TTAAATGATA	120
TGAAGACTAG	GAATGCCAAA	ACACTGACAT	ATTTCGTTA	AAGCCTATCC	AGTCTCTTCA	180
ATTGTATTTG	TAGAAATGCT	ATCAGTAATA	TATTCGCGAA	CACTATGATT	TACAACAGTG	240
TGGTCGTACA	TCTTTGTAAC	TTTATTATAC	AACAACCATT	TACAGGTGTA	AAGTTGAGCA	300
GTGTCTTTAG	TAAATTAGG	GACTTGGTTT	GTCATAGTTT	TGATACCTGT	ATTCTGTTGTT	360
TCATGAGTAT	TTGACGTTTC	TTTCATGTA	GGCATTTCAA	CAATTAGAAT	GATAATTTTC	420
CGAGGATGAA	CTTATATATT	ATGACTTTTT	AGAGTTATGA	TGCCTCTTGA	TTTGACTATC	480
GCTATCAATT	TCATCCACTT	TTACAGTTTC	ATGCAACATA	GCGAGAACGC	GGTTTCCTAT	540
ATGGAAGTCG	TCTTGTGTTTC	ATATTGTCTA	AATACGAGAT	ATTTACTACA	GGTTGTAGAT	600
ATTGCAAGCT	CAAATGATAT	TATTTAGAG	GAGGAGACAA	GTGAAATAAT	GCCTGGTGAG	660
TTAGATGAAA	TAAAAAGTAA	GGAGTTGAAA	GTACTGGTTC	TTTGTGCAGG	GTCTGGAACA	720
AGTGCACAA	TAGCCAATGC	AATTAACGAG	GGCGCTCNAT	TAGCAGAAGT	TAGAGTGATT	780
GCGAATTCAAG	GAGCGCACGG	AG				802

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CTGGGACTCT	CTTCGTAGAA	GTCATGCAAG	AATATTTTGA	TCAAAAGAGG	AAATCATGAA	60
AAAAAGAGCA	ATAGTGGCAG	TCATTGTACT	GCTTTTAATT	GGGCTGGATC	AGTTGGTCAA	120
ATCCTATATC	GTCCAGCAGA	TTCCACTGGG	TGAAGTGCAG	TCCTGGATTG	CCAATTTCGT	180
TAGCTTGACG	TACCTGCAAA	ATCGAGGTGC	AGCCTTTCT	ATCTTACAAG	ATCAGCAGCT	240
GTTATTGCGT	GTCATTACTC	TGGTTGTCGT	GATAGGTGCC	ATTTGGTATT	TACATAAACAA	300
CATGGAGGAC	TCATTCTGGA	TGGCTTGGG	TTTGACTCTA	ATAATCGCGG	GTGGTCTTGG	360
AAACTTTATT	GACAGGGTCA	GTCAGGGCTT	TGTTGTGGAT	ATGTTCCATC	TTGACTTTAT	420
CAACTTTGCA	ATTTCAATG	TGGCAGATAA	CTATCTGACG	GTTGGAGTGA	TTATTTTATT	480
GATTGCAATG	CTAAAAAGAGG	AAATAATGG	AAATTAAAAT	TGAAACTGGT	GGTCTGCGTT	540
TGGATAAGGC	TTTGTCAAGAT	TTGTCAGAAT	TATCACGTAG	TCTCGGAAT	GAACAAATTA	600
AATCAGGCCA	GGTCTTGGTC	AATGGTCAAG	TCAAGAAAGC	AAATACACA	GTCCAAGAGG	660
GTGATGTCGT	CACTTACCAT	GTGCCANAAC	CAGAGGTATT	AGAGTATGTG	GCTGAGGATC	720
TTCCGCTAGA	AATAGTCTAC	CAAGATGAAG	ATGTGGCTGT	CCTTAACAAA	CCTCAGGGAA	780
TGGTTGTGCA	CCCGAGTGCT	GGTCATACCA	GTGGAACCTT	AACTAAATGC	CCCCCATGTA	840
TCATATTAAG	GACTTGTGG	GTATCAATGG	GGTTCTGCCT	CCANGGATTG	TTCACCCGTA	900
TTGATAAGGA	TACGTCACGT	CTTCTCAT				928

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CTCTTTTACA	GAGGTGTTTC	CTATTTTGTG	CTTCCATTGTT	TGGGGCAAGG	AATTGTAGAT	60
GGGGATGGCA	ATCCTATCTT	TTTATTGATT	ATGATATTG	TTTGCTTCAT	AGTTTTAGTC	120

TTTTTGAAAT GGTTAGACTA TGATTTCACT AGATTGAGAA GGGAGTTTCT AGATACAGGT	180
TTTCAAAAGT CTCTTACTAA GATTAACACTGG GCAATGGGG CTTATTATCT AGTGATGCAA	240
AGTCTATCTT ACCTTGAATA TGAACAAGGT ATTCAATCAA CGACTGTTCG CCATCTCATC	300
CTAGTGTGTTT ACCTACTCTT TTTTATGGGG GGTATCAAGA AATTGGATAC CTATTTGAAG	360
GAAAAACTTC AGGAGGAACG GAACCAAGAG CAGACCTTGC GCTACAGAGA TATGGAACGC	420
TATAGTCGGC ATATAGAGGA ACTTTACAAG GAAATTCCGA GTTTTCGCCA TGACTACACT	480
AACCTCTTAA CCACTTACGT TTGGCATTG AAGAGAAGGA TATGGAGCAG ATAAAAGAGA	540
TGTACGACTC GGTCTTAAGG GATTCCAGTC AGAAATTGCA GGACAATAAA TATGACCTGG	600
GCAGATTGGT GAATATTNGT GACCGTGCCTC TCAAGAGTCT CCTAGCTGGA AAATTTATAA	660
AAG	663

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 653 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTAGATTAAT CTGATATTTC TTTTGCAA ACCAAATGCT TCCTATCAGA AAAGCTAGCA	60
ACAGCAACAT GGTAATAATG ATATGAATGG TCATTTCTT CTCCTATTCT GCCTTTCAA	120
TATCTTTTTT CATCTCGTCA ACATTGAAC TAGCAAACAA GTATTGACGG TCTTGGACTG	180
GGAAACGTTG GTCCAACCTGG TCAACTGCTC CCACCTCGAT AATGCCCTTCC TTGATGACAA	240
AATCCATGAC ATGTCCACCG AAGGTCAAAT CATCTGATAT GAAGTGCAGA TGGTAGCCTG	300
CCACACTGAC CCCATGGAAA ATCTCAGGCG TCCAGAAACC AACAAATAGTC CCCGCAACAT	360
TGTCACGACT ATATTCCGGT TGATGGGTTG CGACATCAGC AAACCTGGTA TCGGGTGTG	420
ACTTAGGAAT CATAAGCACA TGCATATGTT AAAAATTCCC CCCCCAATCT TGATAGAGCG	480
GAAAAGATT TCCCCATCAT AATAAGACTC AATTGTTCT TTCAATTCT TGTCTGTCT	540
CTAAAGCGC TGGCGAAAAA TGACCTCTGC CTGATGCGGT ACCACTGCAG CGTAAGGAAT	600
AAGGGCATCT GGTGACACTT CCACAATTTC TGGCTGGTCT CCTGACCCCTT TGG	653

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 989 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTACGATATC TTTGGTCTTT TGTAAGATAT GAGGTCCACC CTTATGCGCC TCAGTTGGCA	60
TTTCATGCGA TTCAAGAAGT TGCCCTCTT GATCAACCAA ACCATACTTG ATGTTGGTTC	120
CACCGATATC AATTGCAACG TAATATGTCA TAAATACCTC CTTTTAGATT AGAGGAAGCG	180
CTCCTTGGTT TCACGAATCA AGGCAGCAGC CGCTTCTACA ACTGGACGAT CTTCTTCAGT	240
CACTGGTGTCA AATGGTGAAC GAACAGATCC AATATTCAAG CCTTCATTGA TTTCAAGAC	300
TTCTTGTATG ACACCGTACA TATTCCATG AGCAGAAGTG AGTTTACCAA TGATTGCGTT	360
GATAGCATAC TGCAATTAC GCGCTGTTTC TAGGTCTTAA TCCGCAATCA ACTGATTGAG	420
TTTCAAGAAG AGTTCTGGCA TAGCACCATA AGTACCCACCG ATACCAGCCC TAGCCCCCAT	480
GAGGCGTCCT CCTAGGAACT GCTCATCAGG ACCATTAAAG ACGATATGGT CTTCTCCACC	540
AAGGCTGACA AAGGTTGGA TATCTTGAAC TGGCATAGAAA GAGTTCTTCA CACCGATAAC	600
ACGAGGATTTC TTCAACATTT CTGTGTAAG GCTTGGAGTC AAAGCAACCC CTGCCAATTG	660
AGGAATGTTG TAAATCACGT AGTCTGTGTT TGGAGCTGCA GAACTGATAT CGITCCAGTA	720
TTTGGCAACT GAGTTATTCT GGCAAGCGGA AATAAATTGG TGGAATCCGT TGCAATAGCA	780
TCTACTCCCCA AGCTTTCAGC ATGGCGAGCA AGTTCCATAC TATCTTGTAGT ATTATTGCAA	840
GCAACATGGG CAATAATGGT CAATTACCT TTGGCTACCG CCATGACTTC TTCCAAAATC	900
AACTTGCAT CTTCAACGCT TTGGTAGATA CATTACCAAG AAGAACCAATT GACATAAGAC	960
CTTGAACACC TTTATCAATG AAGTATTGAA	989

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1671 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TCAAAGAGTA ACAAAAGGCAC CAAATTCTCG ATAGGAACGA TTTAGCACGG TAAACTTCAT	60
CCACTTGGGT TCACGGAACC AAACCAAGCAA TAATTCTTT GGGCACGGGT TAATAGCATT	120
TTGGTCAACT AGGAGTAGAT AGAACACATT TCNTTCTTCG TCTATATCAA TCTTAACACC	180
TGTTTCAGCG ATAATCTTGT CGATGGTTTC TCCACCCCTA CCGATGACAA TCTTAATCTT	240
GTCCACATCA ATCTTGATCG TATCAATTTC CCGGAGCAGTT GGAGCCAATT CTGGACGAAC	300
TTCTGGAATG GTTGCTTCAA TGACATCAAG GATTTCAAAA CCCGCTTCT TGGCTTGAGC	360
AAGAGCCTCC GTCAAGATTT CTGCAAGTAAT CCCTTGAATC TTGATATCCA TTTGAAGGGC	420
TGTAATCCCA TCACGAGTAC CTGCAACCTT GAAGTCCATA TCTCCAAAGT GATCTTCAA	480
ACCTTGGATA TCTGTCAATA CTGTGTTAGTT ATTTCCATCT GAGATAAGTC CCATAGCAAT	540
ACCAGCTACT GGCGCCTTGA TTGGCACACC ACCAGCCATA AGGGCAAGAG TTCCCGCACA	600
GATAGAAGCT TGAGATGAAG AACCGTTGA TTCCAAAATC TCTGCTACTA GACGGATAGC	660

GTATGGGAAT	TCTTCCAAGC	TTGGCAAGAC	TTGAGCAAGA	GCACCGTCAC	CAAGGGCACC	720
GTGACCGATT	TCACGACGAC	CTGGCGCACC	GTAACGACCT	GTTCCTCCCTA	CAGAATATTG	780
AGGGAAAGTTA	TAGTGGTGCA	AAAAGCGTTT	CTTGTACTCT	GGATCCAAAC	CATCAATGAT	840
TTGAGTTCT	CCCATCGGAG	CCAAGGTCAA	GACTGAAAGA	GCTTGAGTTT	GCCCCACGAGT	900
AAAGAGACCT	GAACCATGTT	ACACGAGGAA	GGAAAGTCAAC	AACCGCATCC	AAAGGACGGA	960
TTTCATCGAC	CTTACGACCA	TCAGGACGCA	CTTGTCTTC	TGTAATTAAA	CGTCGCACCT	1020
CTGCGTGTTC	CATTGTTCC	AAGATTTCAAG	CCACATCACG	CATAATACGG	TCAAATTCTT	1080
CGTGGTCCGC	ATATTTTCT	TCGTAAACGG	CAGTCACTTG	GTCTTTCACT	GCTTGAGTTG	1140
CAGTTCACCG	GAATCCAATT	TCTCTTCTAC	TTGAACTGCC	TTTTGGAGGT	CACTGTTGTA	1200
GGCTGCAATG	ATTCAGCTT	GCAATTTCAGC	ATCCACGTGA	AGCAATTCCA	CTTCTGCTTT	1260
TTCTTTACCG	ACAGCAGCAA	CGATTTCTTC	TTGGAAGGCA	ATCAATTCTT	TGACAGCTTC	1320
GTGCCCTTTA	AGAACGCCTT	CCAACATGAT	TTCTTCTGAC	AATTCTTGG	CACCAGACTC	1380
TACCATGTTG	ATAGCGTGCT	TGGTTCCAGC	TACTGTCAAT	TCAAGAAGAG	ATTGCTCTGC	1440
TTGTTCTTGA	CTTGGGTTGA	TGATGATTTG	GCCATCTACA	TATCCCACCTT	GTACCCCAGC	1500
AATTGGTCCG	TCAAATGGAA	TATCTGAAAT	AGACAGTGCC	AAAGATGAAC	CAAACATAGC	1560
AGCCATTGGT	GCAGATGCAT	TTTCATCATA	AGAAAGCACT	GTATTGATGA	CTTGGACTTC	1620
ATTACGGAAA	CTTCCGCAA	ACATAGGACG	AATCGGACGG	TCAATCAAAC	G	1671

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTCAGTATCT	TTGTAATCAA	CATATCCAAT	TTTGTGCT	GCGATGTANT	CAACTTTTTT	60
ACGGCGTTTG	AATCCGCCAC	GACGTNGTTG	AGCCATGTTT	TTCCTCCCTT	ATAAGTTTAG	120
TTGTCCATTA	GAATGGTAAA	TCATCANCTG	AAATACTCAA	TGGGTTTGTT	GCTCCAAATG	180
GATTTCATT	ACGTAAAAG	TCTGGTACTG	AATTGTTAGG	TGCTGAATAG	TTTGCAGTTG	240
GTGCAGAGTA	AGCTCCACCT	GTGTGACCCCT	CACGCACACT	ACGGCTTCC	AACATTTGGA	300
AATTCTCAGC	CACGACCTCT	GTCACGTAGA	CACGTTGTC	TTGCTGGTTA	TCGTAACTAC	360
GAGTCTGGAT	ACGACCTGTC	ACCCCGATAA	GTGAGCCTTT	TTTACGCCCAG	TTAGCAAGAT	420
TTTCAGCCTG	TTGGCGCCAC	ATAACGACAT	TAATAAAATC	AGCCTCACGT	TCACCATTTT	480
GACTCTTAAA	TGTACGGTTT	ACTGCAAGAG	TAAAAGTCGC	AACTGCTACA	TTTGATGGGG	540
TATAACGCAA	CTCAGCGTCA	CGTGTACATAC	GCCCTACAAG	TACAACATTG	TTAATCATAG	600
TTTACCTTCT	TACCGTCAA	TTTGACGAT	CATGTGACGA	AGAATGTCAG	CGTTGATTTT	660
GGAAAGACGG	TCAAACCTT	TAGAGAGCTG	CATCGNTCAT	TTGCTTCAC	GTAAACGATG	720
TGGTAAAGTC	C					731

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 992 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CTGGGTTTTA CCACGTTTTC CTGATGTACG AGCGAGATCC TTACGGTCA ACATAGTGTT	60
GATAAAGCTG GATTACCAA CATTGAAACG CCCTGCTAGG GCAATCTCTG GCAGTTCATC	120
CTGCGGATAG TGGGACTTAT TAGCTGCACT GAGCAAGATT TCAGCATTGT GTGTATTAAG	180
TTCCATAGTC ACCTCTAGGC TGTTCTAGG ATCGGTTTAT CCGTTCCATC GACAGTTTCT	240
TTAGTGTGCA GAACCAATTT CACATTTCC TGACTCGGCA CCTCAAACAT AACATCTAGC	300
ATGGTTCTT CGATGATGGA GCGAAGTCCA CGCGCCCCCTG TCTTCCGTTTC GATTGTTTA	360
TTAGCAATCT CTTGAAGGGC TTCGTCGTCA AATTCCAATC CAACATCATC ATAAGAAAGC	420
AAGGTTTGGT ATTGTTTCAC CAAGGCATTT CTTGGCTCTT TCAAGATGCG AACCAAGTCC	480
ATCAACGGAC AATTGCTCAA GAGCCGCAAA AACAGGCAAG CGTCCATCA ACTCAGGGAT	540
AATAACAAAT TTTTGAATGT CTTCAGCGAT GAATTCTTG ATGTATGAGC TGTTTCTCTG	600
TCAATCGCT TATTGTTTTC ACCAAATCCG ATGACTTTTT CACCCAGACG TTGTTTGACA	660
ATTTCTTCAA TACCATCAA ACCACCCACCC ACGATGAAGA GGATATTTTT TGTATCCACT	720
TGAATCATCT ACTTGTGTG GATGTTGCG TCCACCTTGA GGCAGCACGC TAGAACAGT	780
TCCCTCAATA ATCTTGAGAA GGGCTTGTG CACCCCTTCA CCAGAAACAT CACGTGTGAT	840
AGACACATTC TCACCTCTCT TGGCAATCTT GTCAATTCA TCCACATAGA TAATGCCACG	900
CTCTGCACGT TCGATGTTAA AGTCAGCAAC CTGCAAGAGT TTGAGGAGTA TATTTCCAC	960
ATCCTCACCC ACATAACCAG CCTCCGTCAG AG	992

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ATTTTCACAG GGCAGGATGC GGAACGACTA GCCCCATACT TTAACGGAAT TTTGGTAGGG	60
ACAGCTCTTA TGCAGGCAGA AAATGTGCC CAGAGAAATCA AGGAGTTGCA GATTGACAAA	120

GGTTAAAATT	TGTGGACTAT	CGACCAAAGA	AGCGGTGGAA	ACAGCCGTTT	CAGCAGGAGC	180
CGACTATATC	GGTTTGTCT	TTGCACCTAG	AAAAAGACAG	GTGACTTTAG	AAGAGGCAGC	240
TGAGTTGGCA	AAGCTTATTTC	CTGCAGATGT	AAAAAAGGTT	GGAGTATTTG	TTTCACCAAG	300
TCGGGTAGAA	CTGCTGGAAG	CGATTGACAA	AGTTGGCTTG	GACTTGGTTC	AAGTTCACCG	360
TCAGGTGGCA	GATGATTTAT	TTGAGAATT	GCCTTGTGCC	AGTATTCAAG	CTGTGCAGGT	420
AGATGGAAAT	GGGCATGTCC	CCAATTCTCA	GGCAGATTAT	CTACTCTTTG	ATGCCCTGT	480
GGCAGGAAGT	GGCCAGTCCT	TTGATTGGGG	TCAACTGGAT	ACGACTGGAC	TAGCACAGCC	540
CTTCTTTATC	GCAGGTGGCC	TTAATGAAGA	TAATGTAGTA	AAAGCAATT	AACATTTAC	600
TCCCCTATGCA	GTAGATGTAT	CGAGCGGAGT	GGAGACAGAT	GGACAAAAAG	ATCATGAAAA	660
GATTAGAAGA	TTTATAGAGA	GGGTAAAGCA	TGGCATATCA	GGAACCAAAAT	AAAGATGGAT	720
TTTACGGAAA	ATTCGGCGGA	CGTTTGTCC	CAGAACATT	GATGACAGCA	GTTTTGGAGT	780
TGGAGAAGGC	CTACCGTGAA	AGTCAGGCAG	ACCCAAGTTT	CCAAGAGGAA	TTAAACCAAC	840
TCTTGCGCCA	GTACGTAGGA	CGTGAAACTC	CTCTTTACTA	CGCAAAAAAC	TTGACCCAGC	900
ATATCGGCGG	AGCCAAGATT	TATCTCAAAC	GGGAAGACCT	TAACCATAACA	GGAGCCCACA	960
AGATTAACAA	TGCCTTAGGA	CAAGTTTGGC	TTGCCAAACG	CATGGTAAA	AAAGAAAATTA	1020
TCGCAGAAAC	GGGTGCTGGT	CAGCACGGTG	TGGCAACTGC	AACTGCTGCG	GCCCTCTTTA	1080
ACATGGAATG	TACCATCTAC	ATGGGTGAGG	AAGATGTCAA	ACGCCAAGCC	CTCAATGTGT	1140
TCCGTATGGA	GCTTTTGGGA	GCTAAGGTG	AAGCACTGAC	AGATGGTTCG	CGCCTGCTCA	1200
AGGATGCGGT	CAATGCAGCC	CTTCGTTCAT	GGGTGGCTAA	TATCGACGAT	ACCCACTATA	1260
TCCTTGGTTC	TGCCTTGGGG	CCTCATCCAT	TTCCAGAAA			1299

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1078 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CTGTTGAATC	AAACACACGT	ATCCAAAGTAT	CAGNATCAA	TTATGCAGGT	AATCGTACAA	60
TTGGAAATCA	CCGTGGATGG	TTCAATCAA	CAACAACTTC	TGAAGGTTT	GTTACATATA	120
TTTATGCAGA	TTAATTACA	GAGGGACTCG	AATAGAGCCC	TCTTTTCAGG	TTTTACCGTG	180
ACAATCCCTA	TTAAAAATT	TATCAAATA	GCTTGAAAAT	ATTGGAAAAG	TATGGTAGAA	240
TGAAAATTGT	CGTGTGAACG	ATAATACTC	TTCTTGATGA	ATTGTGAAGC	AGTTGCCCTT	300
GGGTCGTTT	GGCAGTTGAA	GTCAAGAAGA	GGAAAAAAAC	AAAAAGGAGA	AATAACTCATG	360
GCAGTAATT	CAATGAAACA	ACTTCTTGAG	GCTGGTGTAC	ACTTTGGTCA	CCAAACTCGT	420
CGCTGGAAATC	CTAACGATGGC	TAAGTACATC	TTTACTGAAC	GTAACGGAAT	CCACGTTATC	480
GACTTGCAAC	AAACTGTAAA	ATACGCTGAC	CAAGCATAAC	ACTTCATGCG	TGATGCAGCA	540
GCTAACGATG	CAGTTGTATT	GTTCGTTGGT	ACTAAGAAA	CAAGCAGCTG	ATGCAGTTGC	600
TGAAGAAGCA	GTACGTTCA	GTCATACTT	CATCAACCAC	CGITGGTTGG	GTGGAACACTCT	660

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TACAAACTGG GGAACAATCC	AAAAACGTAT CGCTCGTTG	AAAGAAATTA AACGTGGATG	720
GAAGAAGATG GAACTTTCGA	AGTTCTTCCT AAGAAAGAAG	TTGCACTTCT TAACAAACAA	780
CGTGCAGTC TTGAAAATT CTTGGCGGT	ATCCGAAGAT ATGCCTCGTA	CCCCAGATGT	840
GATGTACGTA GTTGACCCAC	ATAAAGAGCA AATCGCATGT	TAAAGAAGCT AAAAATTGG	900
GAATCCCAGT TGTAGCGATG	GTTGACACCA ATACTGATCC	AGATGATATC GATGTAATCA	960
TCCCAGCTAA CGATGACGCT	ATCCGTGCTG TTAAATTGAT	CACAGCTAAA TTGGCTGACG	1020
CTATTATCGA AGGACGTCAA	GGTGAGGATG CAGTAGCCGT	TTGAAGCAGA ATTTGCAG	1078

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CTATGAGGGA TATAAAGTGA GAGAGTTGGG	CCAACGTTCC AAAAACGTCC	TAAATTCTGC	60
CCATTGACAA AGGCAACCCC	CTTACCAAAC TCAGACNAGT	CTAGGTAAGT ATCTTTGGC	120
TATTCGACTG TAAAGTCATA AGCGTAAAG	GCTGGTTGTC	CTTGAGTCCA	180
AAATCAATTTC TCTCAGGATT	GTCTAGTGGG	AGTGGATAGT	240
TGCAGATCCT TACAGACCCC	TGTCGAATT	GTGTCAGATT	300
TGCCCCATAGT TGACACGCC	CATATTTCT	ATCAAGATAT	360
TTTTTACCTT GATAAAAAT	ATCTTCCCCA	ATCTCTGTCT	420
TGACCATCGA CATACTCG	GGCCCTATCT	CGACCATCAA	480
TCTGCATCCC AGTTTGTTC	TGTCGATAA	AGTAGGTAGC	540
TCCATTTT GAGGATAGAG	ACTTTCTACA	GGGACTTGAC	600
CAAAGAAACT TTTCAACTA	GTGGAATAGC	ATCCAACCTCC	660
TTCCAACCTGC GGATACTCTG	AAAAATGTGT	TGCCATCATC	720
AGCAGTTGGA TTTCCTTCTT	CATCCAGAAG	TCATAAGACG	780
GCAGGTCCAA ATTCCCTCGAG			800

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 769 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CTCACGCAGT TCTGTTACCA AAGACCGTTC	AAAAAGCAAA CTAGCAATAC TTATAACTTA	60
TTAGAAAATTC CTAATTTCAC CTTGCTAAC	GAATACAGGT CACCGATGCCA TCTGAGTCTG	120
TGATTTCCAATTCGAT GTCATCCATT TGATTGGTAC	GTCACATTCT TGTGCTCGTT	180
GGGCAATCGT TAACAGTTCT TCTTTATGTG	CAACTTCGAT GACATAGTAG GCTAAACCTG	240
GTAAGCCTTG CTTACGCGGA AGCCAGACCT	TTTCCTCCC CATCGTTAA CTGCTAAATG	300
ATGATGGTAA TCTCCAGCCG CAATCCAATC	AGGCCAGGC ACACATGAATT TATTCTCTAG	360
CCCTAACACC TTTTGATAAA ACTGGCTGGA	CTTTCGACTA TCCTTGACGG AAAGATGAAT	420
ATGCCCTTACCTT CTTGACCTT CTGCCAGGAT	AAAGGGCTCT ACTCTTTCCC CCAACTCATA	480
AATGTCCTGC GCCGCAAGAG CCTCCGTCAC	TCCGATAATG CGTCCATCTT CTCGAATATC	540
CCATGTGGAA ACTGGCTTAT CTCGATAGAG	TTCAATGCCA TTTCCCTCCA AATCTTCCAA	600
GTAAATAGCT TCACTGTAAC CATGGTCTGC	ACCGCCGACA AGAGGAATTT GCAAATCTGT	660
CAGATGTTTC AAGACATCAG CCAAAGCCTT	GGGTGTGGGC AAGAGAATGG CCAAATGGTA	720
AAGACCATAA TGTTCCCTCA CTTCTCCGCT	CTTCTTGTC TTGAATCAG	769

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TTACCCCAAG CCTGCAACTT CCCAAGCTGA	TTGGTTGAAT GATTTGTCAT CAACACCACC	60
AGTATCAGTG ACGATTGCTG CTTTTGTCCTT	CACATCAGAA GATGAAGCTG CGTTACGAGA	120
AGAGCGGTTA CCACATGCAG CAAGTCAAC	TGCTGCCACT GCAACTAGGC CAAGACCTAG	180
CCATTGTTTC TTGTTCATTA CTGAACCTCC	TAATAAGAT GTGCAACGAT GTTGCAAGTA	240
TGGATTGATT GGTCACAAAG ACCCTTGCCA	CTCAAAGAGC GACTCAGACT AATTTAAGTC	300
TGTAAAAGAA TATGGAAGTA ACTCCCCGAC	CGTCATCTCG ACCGTCGATT TATCTTTGC	360
GACTAAGGTC ACTTTTAAAT CTTGTTCAAA	AAATTCGACC ATTACTTGGC GACAAGCACC	420
ACATGGTAA ATCGGTTTT CAGTTTGACC	ATAGACAATC AATTCTGAAA ATTCTCTTG	480
GCCTTCAGAT ATAGCCTTAA AAATAGCTGT	TCTCTCACCG CAATTGGTCC AAAGGATAGC	540
TAGCATTTTC GATATTCACT CCCGTGTTAA	ACATTTCCGT CTTGGCTAC TAAAACGTCT	600
CCGATAGGAA AGTGAGAATA GGGGACATAG	GCATGTT	637

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 940 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CTGAGGATAA	TGACATCTGC	CANAGGAGCA	AAACTAGCAA	AATCATCNGT	TGCACGGTCA	60
ATCATGCCTT	CTTTCAAGGC	GATATCTCTC	GAAGCTTGAC	TACGGATTAT	AACCTAAAAT	120
TTCATAATCT	GGATGATCGC	GTTTGATACC	AAGTGCCATA	GAGGCTCCAA	TCAACCCAAG	180
ACCTGCGATA	TAGATTGTTT	TTGCCATAGG	AACTCCTTAA	TAGTTCTTG	TATAGTCTCG	240
GTGTTGGCT	ACCGCTTCTT	TTAGTTCCCTC	AAGATTATCT	GATGAGAAATT	TTTCGAGGAT	300
TTCTTGCGCC	AGAACCGTTG	CTACAACCTGC	TTCCATGACC	ATTCCCTGCAG	CTGGAAGAGC	360
AGTCGGATCA	CTTCTCTCCA	CGGTTGCCCT	GTAAGGTTCG	TGGGTTTCGA	TATCCACACT	420
CATAAGAGGT	TTATAAAGAG	TAGGAATGGG	TTTCATGACC	CCACGAACAA	CGATGGGTTG	480
CCCATTAGTC	ATACCACCTT	CAAACCACC	TAGATTATTC	GTACGGCGAG	TATAACCGTC	540
TTCTTTAGAC	CAGAGAATT	CATCCATAAC	TTGGCTGCC	TTACGATAAC	CAGCCTCAAA	600
GCCAAGACCA	AATTCCACCC	CTTTAAAGGC	ATTGATAGAG	ACAACAGCTT	GAGCCAATCT	660
TGCATCCAAT	TTTCTATCCC	ATTGGGACAT	AGGAACCAAG	ACCAACTGGG	AACGCCCTCG	720
ACGACTGTCT	CCACAACCCC	ACCGATGGTA	TCACCACAC	GTGGATTTG	GTCAATATAG	780
TCCCTGATTT	CCTGTTCTCG	TTCTTGGTTG	ACAATAGAAA	ACTTCCAGAC	TGGCAGCTC	840
TTTGCTTTAA	TTTCCAGCGA	CTGTCAGATT	TTCCAGGAAC	ATCCATTCCC	TTGCCACCAA	900
AGACCACGAC	ATGGTTGGCA	ATCTCCATAT	CCAGATTGCA			940

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GATTCTACAG	GATCCATT	TTTACTATCTAC	GCGCCGGAA	GTAGGCTGAG	ACATAACCAA	60
GTAATAGAGC	CAACAAC	TAGAGTCTAAA	ACAGATAAAA	GATTTAATT	AAAAACCTTA	120
GTGATGGATG	GGTAAAGTG	ACTTACAATC	GCATTCGCCA	AACTTCCCAC	CCCTTGTGCA	180
ACCAAAATG	CCAGCAGCAA	GGCGATGCC	ACAATCCAGA	TAGCCTCGTA	AATAAAAATT	240
CCTTTGACAT	CACGATTCTG	ATAACCAACT	GCTTTCATGA	CACCTATTTC	CTTGGAACGT	300
TGCATGATAT	TGATGTAAAT	AATGATACCA	ATCATAACCG	CTGCTACCAAC	AATAGCTTGT	360

GATGAAAGCA CAATCAATAA TCCCTGAATA ACACGAATAA AGGTAATCAC AATATCAAGA	420
ACTCTCTGTT AAGAAAGCAC AGTATACTTC TTATTTTCT GTATTCTTC TGTTACTACT	480
TTTGTCTGTG ATGGATCTT GAGTTCCAAG ATAAAATAAG ATACAGCTTT CGTAAATCCA	540
GCCTCTTCA AAATCGTTTC CATTGATGA GACAGCATGA AACTGTTGCT GTCCTCCATG	600
TCATCTTCAT CATTGATTAC ACGTACAATC TTGTTGAA ATTGAGCAAT CTTACTAGTT	660
TGGCAGCAC TTTCTACAAT GCTGACTGAG ACTGATTGTC CAATAAGATC ATTAGCTGTC	720
AAATTTTTTC CTGCTCTGTC ATTCAATT TTAGTAAAG CTGCTTGGAA TCGTTAATCC	780
CTGTTCATTT GTATCAGTAT AGAGGGATCC AGCCAACACT TTGTCGCTC CATTATTACT	840
AACAGAGATA CTTGTATCAT CATAAAGACT CACTACTTGA GCATAAGAAG CATCGTTGA	900
CTCAAATCCA TTTCTTGCCC ATCTTTCTT GCCCATCTAT AGTAATATTG GACATGTTCA	960
TCCCNAAAAGG ACTCTCCAAA TATNNNNATAG	990

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATCGGCTAAC ATGCGTGGAG CATCACAAAT TATCCTATG AGCCGTCATG AAGACGTCAA	60
AAGATGGCTA TGGAGTCAGG TGCGACAGCT GTTGTGAG AACGGTGTCA AGAACGAATT	120
ACCAAGGTGC GTGAAATCCT CGGCGGAGGA GCAGACCGAG CACTTGAATG TGTTGGTACG	180
GAGGCTGCTA TAGAACAGGC GCTAGGTGTT CTTCATAATG GAGGGCGTAT GGGCTTTGTA	240
GGAGTCCAC ACTATAATAA TCGTGCTCTT GGTTGACAT TTATGAAAAA TATCTCTGTA	300
GCAGGTGGGG CAGCTTCTGC TACAACATAC GATAAGCAAT TTTTACTAAA AGCCGTCCTT	360
GATGGTGATA TCAATCCAGG TCGCGTCTTT ACTTCAAGTT ATAAACTGGA AGATATCGAC	420
CAAGCCTACA AAGATATGGA TGAACGTAAG ACCATTAAGT CTATGATTGT AATCGAATAA	480
AAAACGAATA GGAGTTTAG AACTCTATTG GTTTTTATG TTATCCTATT CTTGATTAA	540
GGTACTTTCT CTTAATGTCA GTCTGGTTC CAGCATGGTC AGGCTAGGGAA TTTTCCGACC	600
GTGGAGGACT TCCTTGTAA GAATATCCAT ACCTGCTCGG CCCATTCTT CAGTATAAAC	660
TGTAATACTA AGAGAGGGGA GGATACACCT GTTGGTCAG ACTAAGTGTGTTAAAAGGAA	720
AAATGAGGCT GACCGATCT GGCAGGCTGA TTCCAGCTTC TTGGAGGGCA CGGAGGGCAC	780
CGATAGCTAA ACTATCGCTG GCTGCGAAAA ATGCTGGCGG AAGTTGGTCT CCCAAGCTCT	840
GAATGGCTC CTTCATTAAG TCATAGGCCAG ACTGGGAGT AAATCTTCTT TGAAAGACCA	900
GTTCATCATG ATAGATTCCC CTCGCTTGAC TGTAGTTTT GAAGTTTCTT AGACGCTTGT	960
CCTGAATGAT TTCTTCTTGG TCTGTAGTTT CTTCAAGGCC TGTTAGAATC CCGATAACGGT	1020
CCATTCCCTG ACTGAGGAAA TAATCGACAA CCTGTTCTAT AGCAGTGTAA AAATCCGTGA	1080
TAATACAGGT ATGCCCCAGG GAAAGTGTAT CGCTGTCTAG AAATACAAGA GGCTTTGGT	1140
ATTCTTCAAA GGCAGAAATC TGAGCTTCTT GATAGGATTG ATTCTGCTAG GGATAACAGC	1200

CAAAGGCAAT CCTCCCTTTA TCCACCTCAT ATTTGAAACC ATTTCAGCTC TTA

1253

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CGTGTACCAT CAAGAGGCTA ATTGATGTTT CTTCCCCCTG TGCCTCTCTT GTCAACATTT	60
CTGTTTGAGC CTTATGCGCC TGTATAAAGG CAGCATTGGC ATCAGCTAAT CTTCGATTGG	120
CTTTAGAGAA ATCCCCTTTT TTTGCTGCCT GAATAGCCTC CATAGCATTA CTTTTGGCTT	180
CCCCACCATA CATAATTAGC CCCATTACAG ATTCTAAATT ACTTCATCC ATAACATTCT	240
CCTCAATCTT AGTCTAATAA ACTTTCAGCT AAATCTAAGA CTTTAGAACC ATTCACTCATT	300
CCATAATCTG TCATCGGAAT AACCGCCACA GGAATCTGTC TATCTTTAG TTTTCTTGA	360
AAGTCCCCTA GTAAATAGCG AACTTGAGGA CCTAAAGCA ACACATTTAC TTCTTTTGTGTT	420
GCTACAATTT CTTCTGCTTC AGGAGCTGGA ACTGCAAAA TTTCTGCATC CAACCCCTTA	480
TCTTCTGCTG CTTTTGCACT CTTTGTCACT AGCAGACTTG TACTCATACC TGCTGCACAT	540
GCTAACATAA TTGTTACTTT AGCCATAGCT TACTCCTTTA TCACCTATTT ACTGACCTAG	600
CCAAGCGAGA TACTGTATGT CTCACTCCTC TAATTGCTT GCTCAATGCA TAAATATTAT	660
CGACTGTTGC CAGTCCCCCA TATCCTGCGT CACCTATATG TTGAATATCA ACTCCACAAA	720
TTTTATTTCT AAGTGCAATT TCCTTAATAG TATCTGTATC AGATGTTCT TGGCTAGTAC	780
CAATAGCACT CAATACAAGA CCACCCCTAC TATGAACGAG ATCAACGACT TCACGCAACT	840
CTTGGTCATG AAAGGCTGGA ACGGTCCAA CTGCTGGAAC AAGTATCACA TCCGCACCTG	900
CTTCCAACAA TTGCTCTGCG ACAGAAAGCT CTGCCACAGG CTCATTCACT CCTGCCCCGT	960
GCATCTTACC TGCAATAATC AAACCAGAAA AGTTTCCCTT AGCAGTTGAA ACAGCCTTAA	1020
TGATTTCTCG ATTGCTAACT CCTGTTCCAG GATTTCCAGT CAAACAGACA AAGTCAAAAC	1080
CTAACTCCTA TATTCGCTTC AATGTTCAA CACTAGCAAC ACGACCTGCA ACAATTTCCT	1140
GTGTTTCCCTC TAGCATTCTT TGCAAGATGGG TCAATCGTTT CCAAATTAC ACCAATTGGA	1200
CAAGCAACAA G	1211

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CCACACTAGC AGCCTATGGA CTCACTAAAA GAAAAGAAGA CTAAGTCTTT TCGATAAAAA	60
ATAAACAGCG AGATTGAAGC TCGCTGTTTA TTTTTTAATT AATCACCTAG TCCAAGACGT	120
TCAAAGATAT CATCCACTCG TTGGTGTAA TAAACTGGGT TGAAGATTTTC ATCGATTCT	180
TCTTGTGTGA GACGTGATGT TACTTCTGAA TCTGCCTCAA GAAGTGGTTT AAAGTCTACT	240
TGGTTGTCCTT AAGAGTAGGC TGTTTTGGT TGCAACCAAGT CATAGGCTTG CTCACGGGTC	300
ATGCCTTTT CAATCAATGT CAACATAGCC CGTTGGCTAA AGATAAGACC AAAAGTCGAG	360
TTCATGTTTC GGATCATATT TTCTGGGAAG ACTGTCAACT TCTTGACGAT ATTTCCAAAA	420
CGGTTGAGCA TGTAGTCAAT CAAAATGGTC GTATCTGGTG TGATGATACG CTCAGCTGAT	480
GAGTGAGAAA TATCGCGTTC GTGCCAGAGA GCGACGTTTT CATAAGCCGT AATCATGTGA	540
CCACGAATGA CACGCCGCCAG ACCAGTCATA TTTTCAGAAC CGATTGGTTT GCGTTTGTGA	600
GGCATTGCTG AAGACCCTTT TTGCCCTTTA GCAAAGAACT CTTCTACTTC GCGTTGCTCA	660
GATTTTTGTA GACCACGAAT CTCAGTCGCC ATACGTTGCA TTGAAGTCGC AATGCTGGCA	720
AGAACCGCAA AGTACTCAGC GTGAAGGTCA CGAGGAAGGA CTTGTGTTAA AGATTCCCTTG	780
GGCACGGATG CCAAGTTTAT CGCAGACATA CTCCCTCTACA AATGGTGGGA TATTGGCAAA	840
GTTCCCAACC GCACCCAGAAA TCTTACCCAGC TTCTACACCA GCAGCCGCAT GCTCGAAGCG	900
CTCCGATATT GCGTTTCATT TCGCTGTACC AAGTTGCTAA TTTAAGGACC AAAGGTTGTC	960
GGCTCAGCGT GCACACCAGT AGTTACGCC CATCATGATG GTGAACCTGT GCTCCTTGGC	1020
TTGTCAGCGA TGATATTAGT GAAGTTTCA AGGTACCGAC GGATGATGTC GTTGGCCTGC	1080
TTGTAGAGGT AACCATAACG AGTATCCACC ACGTCGGTAG AAGTTAACCC ATAGTGAACC	1140
CACTTGCCT CTTCACCAAG AGTCTCAGAA ACCGCACCG TGAAAGCCAC CACATCGTGG	1200
CGCGTCTCCT GCTCAATTTC CAAAATACGG TCGATGTCAA AGTCCGCCTT CTTGCGAATC	1260
AAAGCCACAT CTTCCCTTAGG GATTTCCCCA ACTCAGCCCA TGCCCTGTCA GAGAGGATT	1320
CCACCTCAAG CCAAGCACGG TATTTATTTT CTTCACTCCA AATATTCGCC ATCTCAGGGC	1380
GAGAGTAACG GTTGATCATG TGTAAATTTC TCCTTCTTC TTAAG	1425

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CTATTCTGAG TATAAAAGTTG GCGGAGGCTG GAACTACGCT CGTTATGAGG TCATAAAACTA	60
CTATACGGGA GGTTATTAAT CCTTAAAGAG TGAGAAAAGG AGGGCTGGAT ATGTTAAATC	120
TTACTCATGT TACCTTAAAA ACGCGACAAG 'CATCTTGCA AGATGCGGAT TTTACCTTTA	180

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AAAAGGGTAG GATTTATGGC CTTCTTGCTA TCAATGGCTC GGGAAAGACG AACTATTCC	240
GAGCTATGAG CAAGTTGCTT CCCCTTAGTA GTGGACACAT CGCAGTTCCCT CCTTCTTTGT	300
TTTATTATGA GAGCGTTGAA TGGCTGGATG GAAACTTAAG TGGAATGGAC TACCTTCGTC	360
TCATAAAAAAA ACATCTGGAA GTCAGACCTA AACTTGAGAG ATGAAATCGC CTACTGGAA	420
ATGGCTGACT ATATCAGTCT TCCCACCCGC AAGTATTCCCT TAGGGATGAA GCAACGCTTG	480
GTGATTGCTA TGTATTTCT CAGTCAGGCC AAATGCTGGC TCATGGATGA GATTACAAAT	540
GGCTTAGACG AGTATTATAG ACAGAAGTTT TTTGATAGGC TAGCACAAAT CGATAGACAA	600
GAACAGCTGG TTCTTTAAG TTCCCACTAT AAGGAAGACT TGTTGATAT CTGCGATAGA	660
GTAGTAACCA TTCATCAGGG GCAGATAGAA GAGGTTTAGT TTATGAAAGA TGTTAGTCTA	720
TTTTTATTGA AAAAGTTTT CAAAAGTCGT TTAAACTGGA TTATCTTACT TTATTTGCA	780
TCTGTACTCG GTGTTACCTT TTATTTAAAT AGTCAGACTG CAAACTCAGT CAGCTTGGAG	840
AGAGAGTTGG AAACTCGCT TGTAGACCGT GAGAGAGTC ACAATGAAAA TGAAGAGAAA	900
CTCTCCAAA TGTCTGATAC CAGCTCGGAG GAATACCAGT TTGCTAAAAA TAATTTAGAC	960
GTGAAAAAA ATCTTTGAC GCGAAAGACA GAAATTCTGA CTTTATTAAA AGAAGGGCGC	1020
TGGAAAGAGG CCTACTATCT GCAGTGGCAA GATGAAGAGA AGAATTATGA ATTGTATCA	1080
AATGACCCGA CTGCTAGCTC TGGCTTAAAAA ATGGGGTTG ACCG	1124

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1089 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CAGAGCAACT TCGTCAAATC TTCATAGGTG AGGTAACCAA TTGGAAAGAG GTTGGTGGTA	60
AGGACTNACC CATCTCTGTT ATCAATCGGG CAGCCGGCTC TGGCTCTCGT GCTACCTTTG	120
ATACTGTCAT TATGGAAGGT CAGTCTGCCA TGAAAGTC AAGCAGGAT TCAAATGGAG	180
CGGTAAAATC AATCGTATCA AACAAAGTCCA GGAGCTATCT CTTATTTATC TCTTACCTAT	240
ATAGATGATT CGGTAAAAG CATGAAGTTG AATGGCTATG ACTTAAGTCC AGAAAATATA	300
AGTAGCAATA ATTGACCCCTT GTGGCTTAT GAGCATATGT ATACATTGGG GCAGCCCAAT	360
GAGTTGGCTG CAGAATTCTCT CAATTTGTT CTCTCGGATG AGACCCAAGA AGGGATTGTC	420
AAAGGATTGA ACTATATTCC GATTAAGGAA ATGAAGGTG AAAAGATGC TGCCGGAAC	480
GTGACAGTGT TGGAAAGGAG ACAATAATGA ATCAAGAAGA ATTAGCTAAG AAAATGTTGC	540
TTCCATCAA GAATTCTCGT CTGGAGAAAT TAGGAAAGG TTTGACCTTT GCCTGTCTTT	600
CTTTGATAGT CATCCTTG TG GCCATGATT TGTTTCTCGT AGCGCAAAAAA GGCTTGTGCA	660
CCTTCTTTGT CAATGGTGTG AATATCTTGT ACTTTCTTTT GGGAGGAACG TGGAAATCCTT	720
CTAGTAAAGA ATTGCTGCC CTTCCTATGA TTTTGGGTTG CTTTATCGTT ACCATTCTCT	780
CAGCCCTTAT CGCAACACCC TTTGCTATTG GTGCAGCACT TTTTATGACC GAAGTATCAC	840
CAAAAGGGGC GAAGATTTC CAACCAGCTA TTGAACCTCCT GGTTGGGATT CCTTCAGTAG	900

TGTACGGATT TATTGGCTTG CAAGTCGTCG TTCCCTTGT TCGCAGTGT CTTGGTGGGA	960
CTGGTTTGG GATTTGTCA GGGATTTCCG TCCTCTTGT CATGATTTG CCGACCGTAA	1020
CCTTATGAC AACGGATAGC TTGCGTGC GG TTCCTCCNTT ATTATCGTGA AGCCAGTTTC	1080
GCTATGGGA	1089

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CTNTNTMTAA ACCTTGACCT TANTTGANNA TTATACCGAA ATTNTCTTCA TTTTTAAAAG	60
AAAAAAAGGGC GCTGGTAAAAA GGGATAATCT TCACCAACTC CCTATNTTC TACTTATCTA	120
AGCCTAATTC TGCCAAGATT TGACGTTTGT NGGAATCTT TNGGACTTCN TNGTCCTCAT	180
CTTCAGACCA GTCTAGTTTA ATTTCTGAAA CAATCTGCC AGGGNGATTT NTCAAGATAT	240
AGATGCGGTC GCTGAGANTG AGGGCCTCCT CAATACTATG CGTGANGATC AGGGTTGTTA	300
GCTGCACTG CTTGTGAATC TCAAGATACC AAGCGTGGAG TTCCATCTTT GTCATCTCAT	360
CCAAGGCGCT AAAGGCCTCA TCTAAGAGAA AGAGCTTGTG CCCAAAAAGG TAGGTCCGGA	420
GTAAGGCTAC ACGCTGGCGC ATCCCACCGC TAAGTTCATG AGGATACTTG TCTCTTACAG	480
CTGTCAGCTG GAAGGTCGCA AGAATTTAT CCGCTCGGGA AATAGCTTCT GCCTTATCCA	540
CCTTTTGAAT CAAGAGGGC AGAATGATAT TTCCAAGCAC CGTCTTGTGC TCCAAGAGCA	600
GATCCTTTG CAACATATAA CTCACGTGCC CCTTGGGATT TTCTTCACCA TCAAGGACAA	660
TTCTCCCTGA CTGAACCTCT AAAATCCCAG CGATTAGATT AAAGAGGGTG GTCTTTCCAA	720
CACCACTTGG GCCTAGGATG GAAACCACTT CGCCTGAAGT CACCTGTAGG TTGATATCCT	780
CTAAAATCCT CTCCGTACCA TAGGCATAAC TGACGTGCTC TAGTCTAATT TCTGTCAATTA	840
TTTCACAAAT TCGTTGGTGA AGCCTTGTC TGTCAAGTCT TCTTTAAGGA TACCATTTC	900
TTTATCCCCT TTATAGAAAG CATTCAGCG AGCTGCGTCA AATTGACCCCC ATTTTTCCCTT	960
GTGCGTTGCG TATTCTTTG ACAAGTATTT TTGAGATTG ATGACAAAGT CACGTTTTTC	1020
CTTGAGTTCA GGTGCATTCT TGATGAGAAT ATCTGCAGCT TCTNCTGGAT GTTCCATGGC	1080
ATATTGGTAG CCTTTNTGA TGGCTTGGAT GACTTTGCCA GCTTCTTCTT TGTTATCTTT	1140
CAGATAGTCG TTGTTTGCAG TGATAACTGG TGAATATTAN TCAAACCTCT TGACATAGTC	1200
TTTCAANTAC ATGAAGTTAG CATCTACACC TTGAGATTG GCAAGGATAC CATCCCAACC	1260
GTAGTAAATC CNAGCACTAT CAAAGACGCC ATTGGCAATC GGTGTGATTG AGTTTGAGTC	1320
NTTANTTGGT ACTNTTCAA CCTTCTCACA GTCTCCNCT TGAGATTCTA CCAAGGTTTT	1380
CAACATACNN GTTCANTTGG GTCATTCAT GTCCCATATT TCTTACCAAC CAAGTCTTTT	1440
GGACTGCCTA CATTNTCACA TTACCGAGAG ATGATCCCTG ATGTATTGTG TTCCACCNAT	1500
AG	1502

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1022 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACTCTTCAGC GATTCTTGG CTGAGAATGT CCTCATAGGC AGGGAGTTGG ATGTCCTGAC	60
CATATTTCTT CTTGAGGGCA GTAGTAACCA GGCGATAAGC CAGATTGGCA TTACGAGAGA	120
AGATAGGCCG GNNGGAANTAC GAACCAAAGA CATTCTTATA ATGAACCCCT TCACCGACCT	180
TTTCTTCGTT GTTTCCATT CCATAGACAA CCTGTCCCAG CGGTTTTGG TCATCAGAGA	240
GGAAGGTACG ACCTTGGTGA TTTTCAAATC CATAGTAGGT TTCATCGAAA TCTTTCATTG	300
TGAATCTTGA TGTCACCGAT AAAACGGTTA TTGGTCTGGT TGAGCGTGA GTGTCCCAG	360
ACCCCTAGCC CTTCGATAACG TTTTCCTGAA GCTTCAACAT AATATTGACC CAATAGTTGG	420
AAACCACCGC AGATAGCCAG AACTACACCG TCGTTTTGGA TGTAGTTGTC AATGCTCTC	480
TTTTTAGCAG GTAGGTGTC TGCAATGATA CTTTGTCAA AGTCTTGAC ACCACCGAAA	540
AAGGCGATGT CGTAGTGATT TTCATCAAAG TCATCATGGA GAGAAACGAT GTCAACGGTC	600
ACATGGGTTCC CCAAGTTTTC AGCCACATAC TTGAGCATGA GGATGTTCC ATTGTCCCCG	660
TAGGTATTCA TGAGATTTCG GTAGAGGTGG GCAATGTTGA GCTGATAGGG GTAATTGCCA	720
TCTTTTGAGG AAAGTGAAGT ATAAACCATT AGTTCATCTC CTTTCTAACAA ATCTGACGAC	780
TAGCCAGCAG TTCACGAAAT TCCAGCATGG CAGTATAAGT TGCCAGAATA TAGGCATGCT	840
TGCACTCTTG ATTCTCAATG GTCTTGAGAA CTTGCTCCAG ATTACTCGTT TCAGTGATTT	900
TCTCAGCTGG ATAGCCAGTC ACTCGGGAGGC GACGAGCGAT TTCAGAAATGA CGAACACCGC	960
CAGCGTTGAT TTCAGGAATG TCCATGTCAG TGATTGCTC AAAGTCTGCA TCCCAGATCC	1020
AG	1022

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CCTCCAGGTC TCGGGAAACG ACCATGGCCT TTGTTATTGC CAACGAACTG GGAGTCAATC

60

TTAACGAGAC GTCGGGTCCA GTCATTGAAA AAGCCGGAGA TCTGGTAGCT ATTTGAATG	120
AGTTAGATCC TGGGGATGTA CTTTTTATTG ATGAGATCCA TCGTTGCCA ATGTCAGTGG	180
AAGAGGGCT TTATAGTGCT ATGGAGGACT TCTACATAGA TATTATGATT GGGGCTGGTG	240
AGGGTAGTCG TAGTGTTCAT TTGGAGTTAC CACCTTTAC CTTGATTGGT GCGACGACTC	300
GGGCTGGTAT GCTCTCAAT CCGCTACGGG CACGTTTGG GATTACAGGC CATATGGAGT	360
ATTATGCCCA TGCTGACTTG ACAGAAATTG TCGAGCGGAC GGCAGATATT TTTGAGATGG	420
AAATCACTCA TGAGGCAGCA TCTGAGTTGG CCCTACGTAG TCGTGGGACC CCTCGTATTG	480
CCAATCGTCT CCTCAAGCGC GTGCCGATT TTGCCAGAT AATGGGAAT GGGGTAATTG	540
ATGATATTAT TACCGATAAG GCTTTGACTA TGCTGGATGT TGACCATGAA GGTTTGGACT	600
ATGTGGATCA AAAAATCCTT CGTACCATGA TTGAGATGTA CAGTGGAGGA CCTGTTGGTC	660
TAGGAACTCT TTCTGTTGAA TATCGCCGAA GAACGTGAGA CAGTTGAAGA TATGTATGAG	720
CCTTACTTTG ATTCAAAAAG GTTTTATCCA TGCGGACACC GTCCTGGACG GGTGGCGACT	780
GCCTAAGGCA TATGAGCACT TAGGTTATGA ATACAGTGAA AAATAAGCAA GAAATCCTTA	840
GAGGCTTTTT AGAGAAAATC CAGATATGAT GGCCATTCTG ACGATCATCC GAGACCTTGG	900
TCTGAAAGAC TCGTGGTTGG CAGCAGGTTC TGTCAGAAAT TTCATTTGGA ATCTTTTGTGTC	960
AGACAAAATCC CCTTTTGATC ATGAAACAGA TATAGATGTT GATTTCTTT GATCCCAGAT	1020
TTTTCTTATG AGGAAACCTT ATTACTGGAG AAAAGCTGT GAGAGGATTT TCCTCAGTAC	1080
CAGTGGGAAT TGAAAATCA GGCTCTATATG CATCAGCACA GTCCTCACAC TGCTTCCTAT	1140
ACCAGTTCTC GTGATGCTAT GAGTAAGTAT CCAGAACGGT GTACGACAGT TGGACTGCGC	1200
TTGAATGAAG AATCAGATTT TGAACTCTAT GCACCTTATG GTTTGGAGGA TATTTTGAAT	1260
TTCAAGTTCG TCCAACCTCCT CATTCTTAG AAAATGAAGA CGGAATGGAA CTCTATCAAA	1320
CACGTTTATC CAAGAAAAT TGGCAGGAGA AAT	1353

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 560 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CTCCTGGAAA TTCTGGCAAG TAGGCTGGAT GAATGTTGAC AATCCGACCT TCATAAGCCG	60
ACAATAAGGT TGGTCCAACG ATTTTCATGT AGCCTGCTAG GCAAACCAAG TCAATCTGGT	120
GTTCTTCCAA GAGTTCGACA AGGGCTGCTT CGTAGTCTGT CTTGCTCTCA AACTCCTTGA	180
GTTCAAAAGC ATAGGACAGA ACGCCGAGCT GCTTGCACG CTCAAGCACA TAGGCATCAC	240
GATGGTCTGA AAAGACAAAC TCCACTGGAA ATTCTTCGGC AATCACCTGA AAATTTGAGC	300
CATTACCAGA GGCAAAACC GCTATTTTTCATTTGATA ATGACACTTT CGTTTCTTT	360
CTTGACGATG CGACCAATTT CATAGACTGC TTCATCCAAC AATTCTTTA CACGCTCTAC	420
ATTTTCAGGG CTGACCGCCA ACATAAGTCC CACACCCATA TTGAAGATTT CAAACATTC	480
TTCGTGTGTTA ATCTGACCAT ATTTTCAGG GGCTTTGAAA ATTGGAAGCA CTGGAACCTT	540

GCTTCATCA ATTCAGCAG

560

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 860 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTTCAACACT TTATTTTAT CTTCTCCA TTTCGTATGC TAGTCGGAA ATTGTTGCTA	60
GAACCTCTCC GACTATTG GATGTTCTCA TTGCTTTGT AGGAGGGATA GCAGGTATTA	120
TTGGTGTAG GAAAAAAGAG ACCAATAATA TTGTTCTGG TGTTGCTATT GCAACCGCCT	180
TGATGCCTCC TCTTTGTACA GTAGGTTATG CTATTGCTTC TGCTAATCTA AAATTTATCA	240
TTAGGCTCCT CTTACCTATT CCTCATCAAT TGTAGCTTTA TTGTCATTGC GACTTATATA	300
GGTGTAGGT TGATGATGGT TAAGAACAT TATTTTAAAG ATAATGAAGA AGACTCTAAA	360
ATGCGTAGGA TTTTGCTTCT AGTGCTGTT TTGCTGATGA TTCCGAGTTT CATCTCTGCA	420
ACGACTTTAG TGAGAGAAC GTTGAACAC GAGTCCTTA AGAAATTAT ATCAGAGCAG	480
TTTCAGGGGC ATAATATTTT GAAAAAACC TATTCTAAAAG AGACTCATAC CCTAAAGCTA	540
ACCATTTCAAG GAAATTATTT GACAGAAGAA GAACTCGATA TGATTCAAG TAAGAGAGGT	600
GACTATGGTT TAAGTGATGT TTCTGTTCAA GTTTCACAAT TGTCTGATTC AGAACAACTT	660
AGTAAGGAAG AACTGGTGGA GTATTTCTTC CAGTATATCA AGGATAAGGA AGCAAAAGAA	720
AAGGAAAAAG CTAATAAGTT TTATACAGAG TCTGAGGAGC AATAATTCT TGAGAATAGC	780
TGGTTTTCT CGTGAGCTT CTATGTATAT CAAAGGAAGA CTGAGGTTT AAGTATGAAA	840
CTTTTCTTCT ATTATAGTAG	860

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 925 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TCTTGGCCAA CTGCATGGAG TTCAGCGGTC AATTCAACG CACCTGAGAA ACAGACCCCT	60
GCACCCCTGA AATCTCAGGA GACATGATGC TCTGGATGGA ATCAATAATG AGAAAGTCTG	120

GCTGGATACG CTACCACTTC TGCACGAACA CTCTGCATAT TGGTCTCTGC ATAGAGATAA	180
AACTCACTAT CAAAATCACC TAAGCGCTCT GCACGTAGTT TAATCTGCTG GGCAGACTCC	240
TCCCCACTGA CATAGAGAAC TGTCCTTCACT TGGGACAACG GGGTTGAGAC TTGTAGGAGA	300
AGAGTTGATT TCCCCATCCC AGGATCCCCA CCGATGAGGA CGAGACTTTC CTGGTACAAC	360
TCCGCCTCCA AGCACACGGT TGAATTCTC CATCTCCGTC TTGGTTCGAT TGACATTGAT	420
GGAAGTCACC TCAGCTAGTT TCATGGGCTT GGTTTCTCA CCTGTCAAGG ACACACGCGC	480
ATTCTTGACC TCGGCAACCT CAACCTCTTC CACAAAAGAA GACCAAGACC CACAGMTGGG	540
GCAACGTCCC AGATATTTAG GGGATTATA CCCACAATTT TGACATACAA ATGTCGCTTT	600
TTTCTTGTGCG ATGACAAACC TCTTTCTATA TCTCTAACTC AACTCAATC ACTTGGAAA	660
AATCAATCTT CTCATTTGGC ACAAAACTGGC GCATGAGCAT TCGATGAGCA ACAACTACCA	720
CAGTCTGATG TTCTCGATAC TTAAACATAC ATTCTAGAAA CCGAGACTTC ATTTCCGTAG	780
CTGTCTCATA TTGAATAGGA CTATTAGGAA GCAACTCCCC CTTGTTTCT AAAAACAGTC	840
TTCTAGCTGT TTCAAAGTTT TCTATTCCCTG TTTTATAGAC CTGCCATTCA TGTAATAAAG	900
GCTCTACTCT TAAAGGAAGA CCCGT	925

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

TTCTNGATCA AGTCAAGGAC TGCANGCCAC GACCGACATA GCGTTGGCA ATGGAAACAA	60
CCAAACGAAG ATTGGCTTCC GCAAGACGTT GTTGGCTTC GATATGCCA CCTTCACAG	120
CCAGTGCCAA CTCTTCTCC TCTTCATTGG TCAAGAGAGG AACGACCCCT ATTTCTTCA	180
AGTACATACG GACAGGGTCA TTGACCTTAG CAGAAGTTGA CCCAATCAAG TCCTCATCGC	240
TGAGTTCTGG TTCTCTTCA TTGCTAAGAA CACGCCACT TGGATTTCTC TCGTTATCTG	300
TGATAGAAAT GCCTGCATCC TGAATCCGTT GCAAGAGATC TTCATCCCA TCAGCGTCCA	360
AGGTAAAAGG AATAACCAGA CTTGCATTGA TTTCATCATC TGTGCTGTC CCTTTTTGCT	420
TATGATTACG GATAAATTCT GCTACCTGTA CGTCAAATGT TGTTACTTCT TTTTGTGTTG	480
TTGCCATTAT TACTCCATTG TTCTCTTTG GGAAATTAAA CGTTCCAATT CTTCTAGGGC	540
TGTATCTGTA TCTCCTACAT GGCTAGCTTC CTGCACCTTC TTTTGATTG CCATATTGTC	600
CTGATTCAAG AGAGCCTTGT TTGAAAGTCA	630

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CTAGGGCCAT	CTTCTCACCT	CCTCCTTGTC	AGTACATTCT	TGCAATAGAA	AAAATAAGAT	60
TGAGTCCCCC	CAACCTTAAA	TTTTTCACC	ATCTTCTTTT	TCTTTAGCAA	TTTGCTCTTT	120
GATTTCTTT	TCTTCTTCTT	CTTTCGGCG	TTTTCTTCT	TCGATACGGC	GACGCAGTC	180
TTCACGTTTT	CCTTCTGGAT	CTGGGTGAAT	TGTAACGTTT	CCTGATTGCA	TTTCTTCTAA	240
AGCGCGAAGA	GTTGATTTTT	CAGACTTGAA	ACCTTGAGTT	GCTGGGGCAC	CTGCTTCCAA	300
TTCGTGGGCA	CGTTTGCTT	CCAAGATTAC	GAGTGAATAT	TTTGAAGGAA	CCTTGTGAG	360
CAAGGTATCA	ATAGAGGGTT	TTAACATCAT	TTGCTTGTAC	CTATTTCTA	AATTTTATCG	420
GGTAGTTGGA	GATTTGGTA	ACATCTCCTG	ATAGTGCACCA	ATGACACGAT	CCACACAGAA	480
GTGTTCTGCT	TCAATCACAC	ATTTGACACG	TTCAGCAGCT	AGGGGTACCT	GATCGTTGAC	540
AATCGCATAA	TCATACTCAC	GCATGAGGGC	AATTTCTTCC	TTGGCCTTTT	CGATTGTTG	600
GGCAATCACT	TCTGCACTAT	CTGTTCCACG	ACCTACCAAG	CGTTCTGCA	ATTCAATCCAA	660
ATCTGGTGGT	GTCAGGAAGA	AAAGACACGC	ATCTGGAACC	TTTTCTTGA	CCTGAAGAGC	720
ACCCCTGAAC	TCAATTCAA	GGAAAACATC	GATTCCCTTG	TCCAAGGTTT	CATTGACATA	780
GGTCAGAGGA	GGTCCATAGT	AGTGCACG	ATATTCTGG	TATTCCAACA	TCTGTCCTTG	840
ACGAATCAG						849

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GCCAAACAAAC	GCATCCATAA	TGGTTAAATC	TTGATAAGGC	AGAGCTACAT	TCAAAACAGC	60
TTGCTGGTTT	GTAGGTTTC	AATCAGAGCA	ATCACTTCTT	CAACCTTGTC	AGCATCAAGA	120
GCAGCTGTCT	CAATCTTGT	ACTTGTTTG	CCTTCCAGTT	TAGCTTCAA	GTCATCGCAT	180
TTTGACTTGG	TACGGCTAGC	AATCATAATC	TCTGAAATG	TTTCGCTATC	TTGACAAATC	240
TTTGAAATAG	CAACTGGGC	AACGCCCCA	CAACCAATAA	CTAGTAAACG	ACTCATTTTT	300
TTCCCTTCCTC	TTCTTCTAAA	ATGTCCTCAA	CATACTGGG	CAACATAAAG	GCTCCCACGT	360
GTAAGTTG	AGTGTACTAT	TCTGTGAAAA	GCTGGCGTTT	TTTCCAGCCT	TCCTTGTCAA	420
AATCTTTGAC	AGGGTGGTAT	TTTTTCGATG	CAAATCCAAA	CAACCAATAG	CCAGCTGGGC	480
TAGTTGGAAT	ATGGGCCTGA	AAACCCGAC	TGATTGGAAA	GGCTTGATTG	ACCTTGGGGT	540

GCATGCTTCG GCAGGCCGAC TCATCCTCGT CAAAGAAAGG A

581

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TTCTGAAAAT CCATACTTCT ACCAAGGGAGA TACGCTAGCG GTCTCGGAAG TTCTCATACT	60
TCTATCGCTA TATCTGGCCA TCGCCTTCT ATCCAAGGAT TGACAAACAAG AGATAAGGCA	120
GAGAAAAAAAT TCTTGCTGGA TCAGCTGGTT GCCTGCGATG GTGGTACAGG TGTCAATGCAC	180
GAAAGCTTCC ATGTAGATGA TCCGACCCCTC TACTCTCGTG AATGGTTCTC CTGGGCTAAC	240
ATGATGTTCT GTGAGTTGGT CTGGATTAC TTGGATATTG GCTAAGGGGC TCGCTTTAGC	300
TCAACCGATT CTTATCAGAA TCACAAAGTTT ACATTTAAAA CGTTAAAATT TAAATTTAGA	360
ATGAGGTTTT ACTTCATGGA AAATGTTGTT GTACATATTA TCTCACATAG CCACTGGGAT	420
CGTGAGTGGT ACTTGCCCTT TGAAAGCCAT CGTATGCAAT TGGTGBAATT GTTGACAAT	480
CTCTTTGATC TCTTGAAAAA TGACCCCTGAG TTCAAGAGTT TCCACTTGGA TGGACAAACT	540
ATTGTCCCTG ACGACTAATC TACAAATTCG CCCTGAAAAT CGCGACAAGG TCCAACGCTA	600
CATTGACGAG GGCAAGCTTA AAATTGGTCC CTTTTACATC TTGCAGGATG ATTATTTGAT	660
CTCCAGTGAA GCCAATGTCC GCAATACCTT GATTGGCAA CAAGAAGCTG CCAAATGGGG	720
TAAATCAACC CAGATTGGCT ACTTTCCAGA TACCTTTGGA AATATGGAC AAGCGCCTCA	780
AATTCTTCAA AAATCAGGCA TTCACGTGGC GGCCTTGGT CGTGGTGTGA AGCCGATTGG	840
ATTTGACAAC CAAGTCCTTG AAGATGAGCA GTTTACGTCT CAGTTTCAG AAATGTACTG	900
GCAGGGTGTG GATGGTAGTC GTGTTTTAGG TATTCTCTT GCCAACTGGT ACAGTAACGG	960
GAATGAAATT CCAGTGACA AAGATGAGGC CTTGACCTTC TGGAAACAAA AATTGTCAGA	1020
TGTGCGTTGC CTACGCTTCG ACCAACCAAT GGTTGATGAT GAAACGGCTG TGAACACCAAG	1080
CCTGTCCCAA AAAAATCTG AGCGAAGCCA TTCCGTGTGG CAAATGAAC TTTCCGGAT	1140
GTAATCTTTC TTCATAGTTC TTTGATGAA TATGTTCAAG	1180

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CTCAAAAAGT CTGAAATTGG ATCATTGGA ACCATCTGAG CAGTAAGTTT AACACCTTT	60
TCTGCCAGTT TGTGGAAGTC TTCCACATCC TTGTCTACTA CGTTGATAGA ACGTGTAAATA	120
GAACGAGTTT CTGGTGTGG AGACATATTC CCAACATTAA GGGTTCAAG TGGTACACCT	180
GCTTCTACCA AACCAAGGGA AGCGGTCTGG TTTACGAGCC ACGATAAAGA GACGTTGGCT	240
ATCGTATTTG CCAGCAAGAA TATTGGCTGC AGCTTTCTCA ACTGGAAAAA TACTCAATT	300
CACACCTGGT GGTGTCGCAA GTTCAAACC ACTCTTTCA ATATCGTTGT TGACAACATTC	360
GTCGTCTACA ACCATAATGC GTGAAACATT TAGTTTCCA GCCCAAAGAT TGGCTACTTG	420
TCCGTGGATC AAACGTCCAT CAATACGGCA TCCTACAATT GTCATAAGTT TTCCCCCTTT	480
ATATGTTTA GTGTAGGTTT ACGAGTTAA TGAATCTCTT CTTTATATTG ACCTTCTGTT	540
TCAAAGATAA TGATGCGGTT GGCACCTTCC TTGAGATAG	579

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 736 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CGCATANCCT AAAAGTTTTC TTTGACATCT TCTGGAATAT CTGTATCATT AGCTTCCTGA	60
ACATCTCTAC CATAAATCCC AAAGGCTGGA ATCCCTTTT GAGCATGTGA AGCTAGTACA	120
GCTGCAAGAT AGACAGCTCC TGGCGTTCT GTCCCATTAAT ATCCCCAAAT AGCATGAGGA	180
ATATCTGGAG ACATATCCAT AGTTTCACTA CCATAACACC AGCATGGTGT AACTGTAAATT	240
GTTGCGCAA CATTTGATTTC TTAAACAAAC TCATGGGAAG CTGCAGCTC TGGAACACGA	300
CCAATGGTAG ATGGAGAAAT CACACATTCC ACAGGTTCCC CATCTGGATA TTTCAATGTG	360
CTTGAAATCA AATCTGCCAC ACTTTAGCC ATGTTCATG TTTGTACTTC AAGTGATTG	420
CGTACACCTT GACGACGACC ATCAATAGTC GGACGAATCC CAATACGTGG ATGTTGAATC	480
ATACTATTT CCTCTTATTT TTCTGTTCT TTCATACTAC CATGCCATT ATATTTACGG	540
TAGCCTGGGT GACGACCTGT AACCTTATAA TTTTCTCGCA TTGAGAATAG ACGTTCTAAA	600
GTCGGACGAG CAATTCTTG CTCTCAATG CCCTTTGTAG AAAGTAACAT TCTTCCGTGG	660
AAGGTTGTCT TTGCGACTAA TTCTAAAGTT TCCATACGGT AGTATGCTGT AATTACATCG	720
CTTCCGACAG TCAGAG	736

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTCATTGTAT TTAGGAGAAA TGATGGTATC TTCCAAATCA AAATCAACTT CACTCCATAG	60
TCTCAACGGA TTGATTTCC CATCTTGATA GGTCACATCC TTGTCAGGA TAAACTGAGT	120
CAACGCCTCA TGCTGACCTT GACACCTGAT GTCATCTACC AAGAGCCAGA CATCCTCTAC	180
CAACATGAGG ATTTTTCTCT TGTGAAGATA AGGCAAATCA GGTTCTGCTG ACCAATAAGC	240
CCCTTCAATA TAATGCATTC CCTCCCTTTC TTTATGGTGA CAAAACAGGG AGTGAGGATA	300
GTATTCAATAT TCCCAGGATC CGTGATTCT TTCCGGAGCT TTCCCATCTA CAATGCAGGT	360
CGAATGACTC CAAGCACTCT TTAAGAGATA ACGTTCATAT ATCTCCCGAT AAGAATAACG	420
CCCAGCATCT ATGAAAATAG GTTGGCCTTG ATACTGTAAG CAAAAACTAT TCTCGTCACT	480
ATGGCTATGG GCACCTCCTA GCGGACCATT TTTGAAAAAT AGATAACGAT GTTCATCCTT	540
AATGCAGACA TGTCCAGAGT CTTCAAAGAT CATGGACTTA GGCTGCCAAG	590

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CTAGTGTAGC TTCCCTAACAT TTATCTGATA AGATAGCTGT CATATCAGAC TCAATCATT	60
CCTGGAGCAA TCACATTGAC TCGTATATTG CGACTAGCGA CCTCGCGTGC CACAGACTTG	120
GTAAAGCCAA TCAAGCCAGC CTTAGAAGCA GCATAGTTAG CTTGACCAAT ATTCCCCATC	180
AAACCAACAA CACTAGACAT ATTAATGATA GCACCTTCTC TGGCTTCAA TCATCGGTTT	240
CCAAAGACTG ATTGTGTCAAT ATAAAGGCA CCAGTCAGAT TGACCTTGAG CACTTTTCA	300
AAATCTGCTT CTGTCATCTT GAGCATAAGA GTATCTGGG TAATCCCTGC ATTGTTGACC	360
AAAACATCTA CTGAACCCAG TTCTGCAATA GCTTGATCAA TCATACGCTT AGCGTCTGCA	420
AAATCTGATA CATCTCCTGA AATGGGAACC ACCTTGATAC CATACTTGA AACTCAGCG	480
AGCAATTCTT CTGAGATTGC CCCACGACTG TTTAAGACAA TGTTGGCTCC TGCTTGAGCA	540
AACTTGTGGG CGATGGCAAG ACCAATTCGA CGACTCGAAC CTGTAATAAA GATATTTTTA	600
TGTTCTAGTT TCATTTTTT CCTTCAAAA CTTCTACTTA TTTTAGTCTA TTTTTCTAAA	660
AGTGCTACTA AACTCGCTTG ATCTTCCACA TGAGCTAAGT GAGCAGTTG ATCAATTCTT	720
TTAACAAAAC CTGACAAGAC TTTCGGGT CCAATCTCGA ATAAGTTGC TTATGCCCTGC	780

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TTCTTGCATG ACCCCAAATAC TTTCATAGAA ACGAACGGGT TCCTTGACCT GACCGGTCAA	840
GAGCTGAGCA ATGTCCTCTT TTTGCATCAC AGCAGCTTCT GTATTGCCGA CTAGGGGACA	900
AGTAAAATCT GAAAAACTTA CCTGAGCTAG AGTTTCAGCT AGTTTCTGGC TAGCAGGCTC	960
AAGGAGAGCG GTGTGAAAGG GACCTGACAC CTTAAGAGGA ATCAAGCGTT TGGCACCTGC	1020
TTCTTGCAAA AGTTCAACCG CTCGATCAAC TGCAACCCT TCTCCAGCAA TGACGATTG	1080
TGCAGGTGTG TTATAGTTGG CTGGAGTAAC CACTCCAAGT TCCAGAAGCT TTTTGACAGG	1140
CTTCTTCAAT GACCTCTACT GGCGTATTGA GAACTGCTAC CATCTGCCA AGTCAGCA	1199

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CTACTATTTT CTTTGCATA GCCTTCTCCT TTACACACTA CGCATATCGT GGTAAAGAAC	60
ACTGCGTCCC ATCTCACCTG CATTCTCTTT TTGAACAAAG GTATTAGCGT TTATATAGGC	120
AATAGCAGAA GCCTTCAACA CATCAAAATC AAGCCCTGCT GCATTAAGA TGTTTCTGT	180
ATCCCTGTT TCAACAGTGA CCAACAAACCC GATCCTGGC ATCGATTCCA TCTGTTACCG	240
CATTGATAGT GTAGGACACC AAACGAACAG ATTGGTTAAA GAACTTATCG ATAGCGTTAA	300
AGATTGCTTC AACGGAACCC TGTCCCTGTC GCATTAATT CGACTTTCTC ACCATCCATA	360
TTGGCTAGGG TAACGAGCGC TTCAATGTCA TTATCTGCAT GAGTTGAAG TTGTAATCA	420
TCAAAGTGGG AGCCTCTGG ATTTTCAACC ATGGTTCCAG CTACCAAAGC TCGAGTATCT	480
GCATCTGTGA TTTCTTACTT CTTATCGGCC AGTGCCTTGA ACTTAGCAAA GAATGGTTTG	540
ATATCCTCTT CTGAAAATC TAAGGCCAAT TCTCTCAGTT TCTCAACAAA AGCATGGCGA	600
CCAGATAATT TTCCAAGCGG AATCTTAACA CCAACCAATT CAGGTGTGAT GATCTCATAA	660
GTGAGAGGAT TTTTAAGGAC TCCATCTGG TGAATACCAAG ATTCTGGGAA GAAGGTATTG	720
CCACCAACGA CGGTTTGTGTT TTTAGGAACG GGAATACCAAG AGAACCGAGA AACCATTTCT	780
GACGTATTGA TGGTCTCATT TAGGACAATA CTGGTTCTA CTTGGTAGTA ATCTTGGCGA	840
ATATTGAGAG CCACTGCAAT TTCTTCCAAA GCAGCATTTCAGCTCGCTC CCTAATACCA	900
TGGATAGTCT CTTCAAAAG TCCGCACCA TTCTTGACAG CAGCAAGGCT ATTTGCCACT	960
GCCATCCGAA GTTCATCATG ACAGGGAGGC GAATAGATGA TCTGACGATC CGTCTGGACA	1020
TTCTCAATCA GGTATTGGAA GATGGCACCA CATTCTCTG GTGTGGTAAA TCCTATATTTC	1080
TCTGAAAATT TCTTCAGTAA AGAATATTAA GCTAATTGAA AGTCATGAA AATTATTA	1140
ATATTCATT TTTTAGAGGT TAAGTCCAA CTTTTTCTA TCAATTCCAG TACTTNTCA	1200
TCTGATAAAG TATCATCAAG GGACACACTA ATCCAGTAGC GCTTGCTCAT ATGGAAGGCT	1260
GGATAAAATCC CCTTTGTGA AAGCAAATT GCTACTTGGT CATGCTTGAG GTTGACTGCT	1320
TCCACTTGTGTC CTTCTCTGCC CTTTCCAGC TTATTCCAAG AGATTTCAN CAAGACGGCA	1380
TACCACTTTT GATTGCCTTC ATGGCGCAAT ACAG	1414

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CTCCCCATTT	TGGAAAATTT	CTGTCAAGAA	ACGGCGAACCC	AGCTTTTAT	TTTCTGCTTT	60
CTTGTCCAAA	TCCTTGATTT	CAAATCTCC	AAAAATTGGA	TCTAGTTGGT	CATTTTCAGG	120
TGTTCGATAG	TAGTCATGA	CATCCCATA	CTCAACAATA	CGACCATTCT	CATCCGCACG	180
GAAAGTATCC	GTCGTCACCC	ATTGAGCTTC	TCCACCATTTC	AGATATTGAT	GGAACATGAA	240
CAAAGACCAG	ATTGCCATCC	TCAAATGGTCC	GGACAATCTT	AATCTGACGC	TCTGGATGAC	300
GCTCAAAGAA	ATCTGCAAAG	AAGGCTGCAA	ATCCCTTCTT	CCCGTCAGGA	ACACCTGTCC	360
AATGTTGGAT	ATAGGTATCC	CCTACAGACT	GGGCTTGAGC	CTCAGCAACT	CGTCCGTCTT	420
GAATGGCATG	GATGTATAGG	TTGTGAGCAT	TTTCACTTG	TTGTGACATA	TTCTAAACCT	480
CATTTCCCTT	CTCTTTCAGA	TTCGCCAAAA	TTCTTTCTTG	AAAACCTTC	AATTGGTGAA	540
TTTCTTCCTC	TGAAAATCCT	TTGTAAGA	TAGTATCCAA	TTTCTGACTG	ACACGATGCC	600
CCACTTCTTT	CTGGGACTTG	CCTAACTCCG	TTAAAACCAA	ATACTCTTA	CGCTTGTCTT	660
TTCCACACGG	ACTAACAAATT	ACAAGCTTTT	GTTCCCTCTAG	CTTTTTTATC	ATAGTCGTCA	720
CGCTATTATT	CGCAAGCCCA	GTCGCAAGCG				750

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 953 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GTATCGTTCA	ATTCCAAAGA	TACGGAGGAA	GCTGCGTTTC	GCGAGAAAAC	TCTTGTTAGA	60
CCAGATAGGG	ATTAGCCAAA	ATCCCTCTAT	GNGCTTATAT	CCAAATGGAG	ATGCAAACCTT	120
CTGCCCAACT	CTTGACCAAT	AAGATCTTC	TTAAAATCC	ACTCAAGGCT	CTGGTAGAGG	180
AAAAATATGG	GATTGAGTAT	GAAGAATTAA	CCAATCCTTG	GCACGCTGCC	ATTCTAGCT	240
TCGTTGCCTT	TTTCCTTAA	AGTTGCCTC	CAATGCTGTC	AGTGACCATA	TTCCCAAGTG	300

AATATCGCAT CCCTGCTACT GTCCTTATTG TCGGTGTGGC CCTTCTTCTC ACTGGTTACA	360
CTAGTGCAG ACTTGGAAAG GATCCGACTA GAACAGCTAT GATTCGGAAC CTTGCTATTG	420
GTCTCTTGAC CATGGGAGTT ACCTTCCCTGC TCGAACAACT TTTCAGCATT TAGAATACAA	480
GAAATACCTC GATTTTGAAAG TCGAGGTATC TTTTTTACAT TTGCACAATC TTGCGATAAC	540
TTCTTGAACT AATCATGAAA ATCAGCACAT AGGCGATGAG GAAGATAGCG CAGATAGACA	600
AGGTCACAAT CAACATCATA GTCGTATCCA GTACACCAAT CACTTTAAA ATCAGGCTAA	660
GCATATGGTA GGCAGGCG AGATGTATGA AGGCAAAGAG CAAAGGAAGG AAGAAAACAG	720
TTAAAACCTG TTTGTTGATG GTTGTCTGAA TTTGCTTTG GTCCAAACCG ACTTTCTGCA	780
AGATAATAAA GCGTTCACGG TCTTCGTAGC CTTCAGAAAT TTGTTTGTAG TAGATGACCA	840
GAACAGTTCC GACCATAAAAG ATAATGGATA GGAAAATACC GATAAAGAAG ACACCGCCAA	900
AGAGGACACT CATTGAGCA CTAGCATCTG CTAGATTGCT ACCATAAACAA TAG	953

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CTGATTGAACTTCTATTTCATAATATTCAA AAATCCTCCG TTTCAAAGAG CAGGGAACTC	60
TTTGTGACAG AGGATTTTCTATAGGGCT TTAGCAGCTG CAATTGCGGC TTCGAAGTTT	120
GGCTCAGAAAT TGATATTATC CACGTATTCA ACGTAGCGAA TCGTATTGTC AGTATCGAGG	180
ACAAAGACTG CGCGTGCTAA TAGGTGCCAT TCGTTGATCA AGAGGGCATA ATCGCGCCCG	240
AAAGAATGGT CAAAGTAGTC TGAAAGCATA ATGGCATTGT CAAGGCCTTC AGCACCGCAC	300
CAACGTTTTGAGCAAAAGG TAGGTCCATT GAAACAGTCA ATACGACCGT GTTGTCCAGT	360
CCAGCCAATT CTTCATTAACCGACGTGTT TGAGTTGAGC AGATGCCTGT ATCGATAGAA	420
GGAAACGACAC TCAAGACTTT TTTCTTGCCA TCAAAATCAG CCAGAGATTT TTTAGAAAGA	480
TCTGTTGAG TAAGAGAAAA ATCAAGCGCC TTGTCGCCGA CTTGTTGTTG TTTACCTGTA	540
AAGCTCACAG GATTTCCGAG AAAAGTTACC ATAGGATACT CCAATCTTTT TTCTTCCATT	600
GTATCTGAAA CAGTCAGAAATTTCATGA TTGACCGGA AATGTGGCA TAGAAAAAAC	660
GCCAG	665

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1039 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CTAAGTATAA AAAACTTGCC GAAAGTATCT CTGAAGTTAA TTTGAATGTC	TTTTTTCAAA 60
ATGCTTAGA TTTTGTGAA ATCTTAATC AAGAGCCTTG TCTGATAAAT TTTTTGAGT	120
TTATGAATTC TATGTTACAA GGCGATATT CAAAGTTAAC AATAAACCAA GAATAATAAG	180
AGGGGAACAG TATGAAAGAT ACGATTCTA ATAAGGATT GATTCCATG GGCTATAGAC	240
CATCAACAGC AAATGCTATT ATCCATCAGG TGAGAGAATT ACTTGTATCA CGAGGCTATA	300
CATTTTATAA TCGCAAACGT TTGATGGTTG TTCCAAAAG TGTTGTGAAA GAGTTGTTGG	360
GAATGGAATT GTGAAATGGC TTATATCGAG TATAAACAGC GTGGGAAGAA AAGGCTTGG	420
TCGTTTCTA TACGTGAGAG GAGCAAGAGC CTACTCCATA AAAGCGGATT TAAAACAAAA	480
CGAGAAGCTA AAATAGAAGC GGAGAAAGTT CTTCTATAAGT TAAATACTGG GAGTGTCTTA	540
AGCTCTAGTA TGACTTTATC GGAGCTTAT AATGAATGGC TGGATTTAAA AATTTTACCT	600
AGCAATAGAA GTGTAGTTAC TAAAAAAAAA TATCTTATGA GAAAGAAGGT CATCGAAAGG	660
TTATTTGGAA ATAAGCCTGT ATCACAAATT AAGCCTAGCG AGTATCAAAA AATTATGAAT	720
GAGTATGGAG AGACTGTATC GAGAAATTTC TTAGGAAGAT TGAATTCTAG TATCCAGGCA	780
AGTATACAGA TGGCTATTGC TGATAAGGTG ATAATAGAGG ATTTTACTGC TTATGTTGAG	840
TTGTTCTCTT CTAAGAGTGG ACACAAAGGT TGAGGAAAG TATCTACATA CTGAGTCAGA	900
TTATCAAAAA GTTTTAGTAT ATTTGAAAAA TAAGTTGAT TATCAGAAAT CTATTGTACC	960
GTATGTAATT TATTCCTTT TTAAACTGG CATGCGTTTC TCCGAATTGA TTGCTCTAAC	1020
TTGGGATGAA GTTGACGAG	1039

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CTGAGAAGTC AGGAAGGCCA TGTGGAGAGA TTGAGGAATT GGATACTTAA CTCCATAGTA	60
ATCTTCGTA AACTCGATAG AGCGAACAGC GATATCCAGT GAGAAATCAA GATTGAAAG	120
TGGATGTGCT TTGGTTGAGT AGACACCCCA CCAGGGTACC ATTTTTAGTT TTAGCGGTCA	180
CCCCTTGCAA ATCACCAAGCA ACAAAAGGCCA ACAAGTAAGA AGACATGCGA GGTGTTGTCT	240
CAAACCTCCA GATACTGTT TCCTTACGGT TTTCAACATC GATTCTGGC ATGTTTGACA	300
AGGCCAATTC ACCTTCTGCT TGGTCAAAGC GAAGAGAGAG GTCAAAAGTT GCTTTGGCTT	360
CAGGCTCATC CACACATGGG AAAGCTTCGC GCGAAAATG GCTCTCGAAC TGAGTAGACA	420
AGACCTCCCTT CTTGACTCCA TCAACTGTAT AATAAGAAGG GTAAATCCCT GTCATGTTGT	480

CTGTAATTTT ACCAGAAAAG GCAAGAACCA ATTCAACTTG ACCAGCCTCA GCCAATTGCA	540
TATGAAGGGC TTCATGTCA TGGTCAACTG TAAATGGACG AGCTTGACCT GCAACTTCTA	600
CAGAGGTGAT TTCCAAGTCT TTTGGTGG A GGAGATGCG GTCACTCTGT GCTTGACCAG	660
TGATGGTCAC TTTCCCAGAA AAAGTCTTGG TCTCACGACT CAAATCTAAA AATAAATCAT	720
AATGTTCAAG AACAATTGC TTAATAAAAT GTTCAACTGC TTGCATAGTT TTCTCCTATT	780
CTAAAGTTAA GAG	793

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CGGATGATTT GCTTTTCATC TATGATAAAAG TCTTTGTTGA GCGTCGGAAT CTCTACTGAC	60
TGGAAATTTC CCGTAGATAAA TCCAAATGCC CTTTAAAGAA AACCTCATCT GTCAACACCG	120
AAATCATCAC TGCTCCGTTT TCTTCATAAG TCTGGGCTG TTGCACAATA TCCACATCGA	180
GATTGATATC TCCCCAAAAC TAGGGCTAGC TTTCTTGACT TCAGGGATTA CCTGCAAGCG	240
GTCCCTGATGA TTCTTCAAAA ATTCTGCCAA GCGATAGGTC TGGCGCAGAG GCTGGATTTG	300
CTCCAGCTTC ATCTGCTCCA CCTCACGCGC CTTCTGCTCT AAGATTCGTG CTAAAAATTC	360
CTGACTCATT TTTGGTACTC CTGTAACAGT CTGAGTTTTT CAAGGGCCTT GCCTCTAGCA	420
ATCACTTGAC GGGCCAAGGC AACTCCTTCC TTGATGCTAT CAATCTTACC ATTAGCATAG	480
AAACCAAGAC CAGCATTCAA GACTGTCGTT TCCAAGAATG GACTTGCTTC GTTTTCAGA	540
ACGCTAAGCA AAATTTCTGC ATTTTCTGA GCATTCCCAC CACGAATATC TTCCATAGCA	600
TAGCCTTCCA TTCCCAAATC CTCTGGAGTA AAGCTTGACA AG	642

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 733 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CTCTTGAGG TTATTAAGGA GAAAACGGAG GTAATAGAAG TATGATTTAT ACAGTCACAC	60
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TCAATCCATC	CATTGACTAT	ATCGTTCGTT	TGGACCAAGT	CAAAGTTGGT	AGTGTAAATC	120
GTATGGACAG	TGATGATAAAG	TTTGCTGGTG	GGAAAGGAAT	CAATGTCAGC	CGTGTCTTGA	180
AACGTTGAA	TATATCAAAT	ACAGCGACGG	GATTTATCGG	TGGCTTTACT	GGTAAATTAA	240
NCNCAGATAC	TTTAGCAGAG	GAAGAAATCG	AGACNCGTTT	TGTCCAGGTG	GCAGAAGATA	300
CTCGTATCAA	TGTTAAAATC	NAAGCAGACC	AAGAAACAGA	AATCAACGGA	ACGGGTCCAA	360
CTGTTGAACC	GGTTAACGCTA	GAAGAATTGA	AAGCTATTTT	ATCTAGTCTG	ACAGCAGAAG	420
ATACAGTTGT	CTTTCAGGT	TCAAGTGTCA	AAAATCTAGG	CAATGTTATC	TATAAGGGAT	480
TTAATCTCCT	TGACGCCCA	GACTGGTGCG	CAAGTGGTCT	GTGACTTTGA	AGGACAGACC	540
TTAATTGATA	GTGTTGGATTA	CCACCCCTCTT	CTTGTAAAC	CAAATAATCA	TGAACCTTGGA	600
GCGATTTTG	GGGTTAAACT	CGAAAGTTA	GATGAAATTG	AGAAATAACGC	TCGTGAGTTA	660
CTGGCTAAGG	GTGCTAAAAA	TGTTATTATC	TCTATGGCTG	GTGATGGTGC	CCTTCTTGTC	720
ACATCTGAGG	GAG					733

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CTAAGGGAAG	TAGGAAAAGT	ATGTATCCAG	ATGATAGTTT	GACATTGCAA	CACGGACTTG	60
TACCAAGATCA	ACATGATGCA	GGTTTACTTT	GATCAAGGGA	TTTACAATAA	GAAGGCGGTC	120
TTTGAGGTGT	ATTTCCGCCA	ACAGCCTTTT	AAGAACGGCT	ATGCGGTTTT	TGCAGGTTTG	180
GAAAGAATTG	TGAACATATCT	TGAAGACTTG	CGTTTTTCAG	ATAGTGTATAT	AGCCTATTTG	240
GAGTCGTTG	GTTATCATGG	GGCGTTCTTG	GATTACCTTC	GCAATTCAA	GTTGGAGTTG	300
ACCGTTCGTT	CTGCCCAAGA	AGGGGATTG	GTGTTGCTA	ATGAACCGAT	TGTGCAGGTG	360
GAAGGACCTC	TAGCCCAATG	TCAGTTGGTC	GAAACGGCTC	TTTGAAACAT	CGTCAACTAC	420
CAGACCTTGG	TGGCGACGAA	GGCAGCCCCC	TATCCGTTTG	GTTATCGAAA	ATGAACCCCTT	480
GATGGAGTTT	GGGACACGTC	GGGCTCAAGA	AATGGATGCG	GCCATCTGGG	AACACG	536

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CTGCCCCCTGT AAGGCTGGAC GATTGCCCTT CTTAGTATCC GCAAAGAGGT AACTGAGAA	60
TAGAGAGGAT TTCTCCTTCAT ATATCTTGACAGACAGGTT CATCTTGCCT TCTACGTCTG	120
AAAAAATCCG CATATTGACC AGTTTCTCA CAGCATAGTC CAAATCTTCC TCTTGGTCCT	180
CTGGTCCAAC ACCAACCCAGC AATAAAAGTC CCTGATTGAT TTTCCCTGA ATCTGGCCTT	240
CTATACTCAC TTGGGCTTTT TTAACCCGTT GGATAATGAT TTTCATAATA GCCTTCTAG	300
TAAGAGCTAG GACAACCTAGC CGTGGTCCG TTTGACAGAG TAAACTCTG GCACACTCTT	360
AATTTTATCG ACAACCGTGG TCAGTGTAGA GAGGTTGGCA ATACCGAAGG ACACATGGAT	420
ATTAGCAAAC TTCATATCCT TGGTTGGTTG GGCATTGACC GTTGAATAT TCTTGGTTGT	480
ATTTGAAAGA ACTTGCAGTA CATCGTCAA CAGTCCTGTA CGGTTGAGAC CGTAGATATC	540
GATATGGGCC ATATACTCCT TATTGAG	568

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CTTTATATTG TACCAAGTAT CATTCTAGT GCTGCTATGG GCTTGATTTT TCTTCAAATC	60
TATAATCCAA ACTATGGTGT TGTTAACCAA ATTATTCACT TATTTAATCC ATCGTTAAA	120
GATTCAGTAC TGTTGACTCC CAGGATTAAA AATAGTAGCT ATGACTGGCG CTTATATCTT	180
CTTTGCAGGA GCATCAACCA TTATGATTTC TTGGGCAAAT TTTGCTATT CCAGAAGAAG	240
TTCAAGAACG TGCTATTTTA GACAATATTA CTGGTTGGAG GAAAGAGTGG TATATTACGA	300
TTCCGATGAT TAAGGGACA ATTAAAATG TTTCAATTAT GGCACCAACT TCAGGATTTT	360
TGCTCTATAA CGAAGTATTTC TTTTGACAA ATGGTGCCTG AGGAACAAAA AGTATCAGTT	420
TTGTTATTG AGAATTAGCA GTGGCTAGCT CACGAACCTCA GTATGCTCGT GCAAATACAA	480
TTGGAGTTAT ACAAACTTAA GGTGGAATGT TGATTATCGT TTGTTATTAAT ATTTTATTC	540
GAGAAAGAAA AAGACTGAAA GGTGGGAAAT GATTATGAAT ACACATATAA ATGGTATTAG	600
TAAAAAAAGGC AAAGTTCTTA TATATGGTTA TATGCTCCTT ACCATTTAA TTTCTATTTT	660
CCCTATTGCG TGGATTTTT TATCATCATT AAAAGCAGAT CCTATGAAAA ATCCAGGTAT	720
TAGTTTACCG ACTGACTTTA CTCTTGAAGG TTATATAAT GTTTTACAA AACTTCATGT	780
TTTTACTTAC TTTTGAATA	800

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CTCAGTATTA	TCCCTACCAA	AATGAACGTC	AGTTAGTGAC	TCAGGTGGTT	TGGGAACAAT	60
GGGTTTGG	ATTCCAGCAG	CAATCGGTGC	AAAATTGCT	AACCCAGATA	AGGAAGTAGT	120
CTTGTGTTGTT	GGGGATGGTG	GTTTCCAAT	GACCAACCAG	GAGTTGGCTA	TTTTGAATAT	180
TTACAAGGTG	CCAATCAAGG	TGGTTATGCT	GAACAATCAT	TCACTTGGAA	TGGTTCGCCA	240
GTGGCAGGAA	TCCTTCTATG	AAGGCAGAAC	ATCAGAGTCG	GTCTTGATA	CCCTTCCTGA	300
TTTCCAATTG	ATGGCGCAGG	CTTATGGTAT	AAAAAACTAT	AAGTTTGACA	ATCCTGAGAC	360
CTTGGCTCAA	GACCTTGAAG	CTACTACTGA	GGATGTTCCCT	ATGCTAATTG	AGGTAGATAT	420
TTCTCGTAAG	GAACAGGTGT	TACCAATGGT	ACCGGCTGGT	AAGAGTAATC	ATGAGATGTT	480
GGGGGTGAAG	TTCCATGCGT	AGAATGTTAA	CAGCAAAC	ACAAAATCGT	TCAGGAGTAC	540
TCAATCGCTT	TACAGGTGTC	CTATCTCGTC	GTCAGGTTAA	TATTGAAAGC	ATCTCTGTTG	600
GAGCAACAGA	AGATCCGAAT	GTATCGCGTA	TCACTATTAT	CATTGATGTT	GCTTCTCATG	660
ATGAAGTGG	GCAAATCATC	AAACAG				686

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 802 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TTTTCCCAGC	TATTTTACTG	AGTATAAAAG	CCTTATTAA	CTTACTCTAT	GTACTCGGTT	60
TTCTAGGAGG	AATGTTGGGA	GTTGGGATIG	CTTGGGGTA	CGGAGTGGCC	TTATTTGACA	120
AGGTTGGGT	GCCTCAAACA	GAAGAATTGG	TGAATCAGGT	CAAGGACATC	TCTTCTATT	180
CACAGATTAC	CTATTCGGAC	GGGACGGTGA	TTGCTTCAT	AGAGAGTGAT	TTGTTGCGCA	240
CTTCTATCTC	ATCTGAGCAA	ATTTCGGAAA	ATCTGAAGAA	GGCTATCATT	GCGACAGAAG	300
ATGAACACTT	TAAAGAACAT	AAGGGTGTAC	TACCAAGGC	GGTGATTCGT	GCGACCTTGG	360
GGAAATTGT	AGGTTGGGT	TCCTCTAGTG	GGGGTTCAAC	CTTGACCCAG	CAACTAATT	420
AACAGCAGGT	GGTTGGGGAT	GCGCCGACCT	TGGCTCGTAA	GGCGGCAGAA	ATTGTGGATG	480
CTCTTGCCTT	GGAACGCGCC	ATGAATAAG	ATGAGATTT	AACGACCTAT	CTCAATGTGG	540
CTCCCTTGG	ATCGAAATAA	TAAGGGACAG	AATATTGCAG	GGGCTCGCA	AGCAGCTGAG	600

GGAATTTTCG GTGTAGATGC CAGTCAGTTG ACTGTTCTC AAGCAGCATT TTTAGCAGGA	660
CTTCCACAGA GTCCCATTAC TTACTCTCCT TATGAAAATA CTGGGGATT GAAGAATTGA	720
TGAAGACCTA GAAATTGGCT TAAGACGGGC TAAGGCATTTC TTTACAGTAT GTATCCTACA	780
GGTGCATTA GCAGAACAA TT	802

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTACTATTT AGCATAAAAA TGCCCAAAGG GGGNGCCGTG TGTTCAGGNT	60
AATGGACCAG GNAAATCAGC ATGAAAATAA AAAGAGAAAC AGATTATTTT AGCCATTGTT	120
CAGATTTATG CTATGCTTAA GGTAGAAAAT GAAAGGGATA ACAAAATGTAT TTAGGAGATT	180
TGATGGAGAA AGCCGAGTGT GGTCATTTT CAATCCTTTC CTTTCTATTAA CAAGAGTCTC	240
AGACGACCCT CAAGGCTGTA ATGGAAGAAA CAGGATTTTC AAAAGCAACC CTAACCAAAT	300
ATGTCACCCCT GCTCAATGAC AAGGCTTGG ATAGTGGCTT AGAACTGACT ATTCACTCAG	360
AAGATGAAAA TCTGCGTCTG TCTATAGGTG CAGCTACTAA GGGGAGAGAT ATTCCGGAGC	420
TTGTTTTTTG GATAGTGCTG TTAAATACCA GATTTGGTT TATCTTCTCT ACCACCAACA	480
GTCCCCAGGCC CATCAGCTGG CTCAAGAATT GGTGATTAGC GAGGCTACGC TTGGTCGTCA	540
CTTAG	545

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAGGTCAAGA TTGATTCCCA AGGTTNGAGG AATCTGGGA ACCAGATTAA GAAGAAATCG	60
AGCGGTTACC ATGCTTGGCC ATGTGAATAC CGCCACCAGC CAAGACAAAG CCTGCAGTTG	120
TGGAAATATT AAAACTGAAA GACTTGTCCC CACCTGTACC ACAGTTGTCC ATAGCATCAT	180
GAATCTCAGT TCCAATATGC TG/GGCAATTC CTCTCATGAC TTGGGCAATG CCTGTGCGTT	240

CTTCAGGTGT TTCCCCCTTC ATCTTAAGAG CTAAGAGGAG AGAACAAATC TGCCTTCAG	300
TTACACGCC AGTTACGATA CGCTCAATGA CATCCGTCAT TTCCACACCT GATAAATTTC	360
CAAATTTTGC TAGMTTTCA ATAATCTCTT TCATCCTAGT TTCCTCACTT TACAACCTCC	420
TCGATAAAAT TCCGAATAGA AGACAAGCCG TCTGGCGTTC CAATGCTCTC TGGATGGTAC	480
TGGAAGCCAT AAATCGGTAG GTTTTATGT TGAATCCCCA TGATGGCTTG GTCATCAGTC	540
GAACGAGATC AAGCTTATCG ATACCGTNGA CCTCGA	576

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATTAAGGGA GGCGAACATG GCCCAAGATA TAAAAAATGG AGAAGTAGAA GAAGTTCAAG	60
AAGAGGAAGT TGTGGAAACA GCTGAAGAAA CAACTCCTGA AAAGTCTGAG TTGGACTTGG	120
CAAATGAACG TGCAGATGAG TTGAAAACA AATATTCTTC GCGCTCATGC AGAAATGCAA	180
AATATCCAAC GCCGTGCCAA TGAAGAACGT CAAAACTTGC AACGTTATCG TAGCCAGGAC	240
TTGGCAAAG CAATCTTACC ATCTCTTGAC AACCTTGAGC GTGCACTTGC AGTTGAAGGT	300
TTGACAGATG ATGTGAAGAA GGGCTGGGG ATGGTGCAAG AAAGCTTGAT TCACGCTTTG	360
AAAGAAGAAG GAATTGAAGA AATCGCAGCA GATGGCGAAT TTGACCATAA CTACCATATG	420
GCCATCCAAA CTCTCCCAGC AGACGATGAC CACCCAGTAG ATACCATCGC CCAAGTCTTT	480
CAAAAAGGCT ACAAACTCCA TGACCGCATC CTACGCCAG CAATGGTAGT GGTGTATAAC	540
TAAGATACAA AGCCCGTAAAGCTCGCAG TAAAAATAGG AGATTGACGA AGTGTTCGAT	600
GAACACAAGA AAATCTANCT TTTTACTCA GAGCTTAGGG CGTGTTCGAT TCGGCAATTG	660
TGACGGTAG	669

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

CTAGTTCA	60
CTAATTCG	120
GAAATACACC	180
GAAATATCAT	240
ATAAGGTAAA	300
ATCCTTATT	360
AGACCGATAA	420
ACCCATACTT	480
CAGAGATACT	540
TCCTCTGAA	600
ATTTAGAGTA	615
ACTCTTATTA	
GACATTTGAT	
GTATCGTTAT	
CGGGCTATT	
GAAGGAGCCC	
GATTTAAAC	
TTCTTTATT	
ATGAAATTTC	
TCCTTC	
AAAAACAT	
TCTATATACT	
TAAATTTAG	
GGCAAGACTG	
CCGTTCCACT	
GACCACGCTC	
CACTTGCCAG	
CAAAGCTGGC	
AGGTCCAGCC	
TTACCC	
TTAACATTAT	
TTAATTTTG	
CCATTCAAT	
CAATTCTGCA	
AAGGTCCCAA	
GCTTCTGGA	
TTGAATTACC	
TCATATTGGG	
CATTCTGTCC	
AAATGAAGCA	
TTATTAATCA	
CTTCACCTC	
ATAAAGGCCT	
GGAGCAGAGA	
AAACAGCTCC	
AAATTGGAT	
TTATCGAAAT	
GCATACCTAG	
GTCACTCCAA	
CAATCATTAA	
GGGTGGAGAC	
TTTTATCCAG	
CCTCGTTCTT	
TCTTAGTAGA	
AATAG	

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CTACTGTAGT	60
TGGAACTGTT	120
GAAAACAAG	180
GAAAACAAAA	240
GAAAGTTGTT	300
ACTTACAAGT	360
ACAAACCTAA	420
AAAAGGTAGC	480
CACCGTAAAC	540
AAGGTACCG	600
TCAACCATAT	660
ACAAAAGTTG	720
TCATCAACGC	773
AATTAACGCT	
TAATTTAAG	
GAGAACACAT	
GATACAAGCA	
GTCTTTGAGA	
GAGCCGAAGA	
TGGCGAGCTG	
AGGAGTGCAG	
AAATTACTGG	
ACACGCCAG	
AGTGGCGAAT	
ACGGCTTAGA	
TGTCGTGTGT	
GCATCGGTTT	
CTACCGCTGC	
CATTAAC	
ACTTT	
ATCAATTCTA	
TTGAGAAATT	
TGCAGGCTAT	
GAACCAATCC	
TAGAATTAAA	
CGAAGATGAA	
GGTGGCTATC	
TGATGGTTGA	
AATACCAAAA	
GATCTTCCTT	
CACACCAGAG	
AGAAATGACC	
CAGITATTCT	
TTGAATCATT	
TTTCTTAGGT	
ATGGCAAAT	
TATCGGAGAA	
CTCTCTGAG	
TTCGTCCAAA	
CCAGAGTTAT	
CACAGAAAAC	
TAACACGGAG	
GAAAACATTA	
TGTTAAAAT	
GACTCTTAAC	
AACTTGCAAC	
TTTCGCCCA	
CAAAAAAGGT	
GGAGGTTCTA	
CATCAAACGG	
ACGTGATTCA	
CAAGCGAAC	
GTCTTGAGC	
TAAAGCAGCT	
GACGGACAAA	
CTGTAACAGG	
TGGATCAATC	
CTTTACCGTC	
AACGTGGTAC	
ACACATCTAT	
CCAGGTGTAA	
ACGTTGGTCG	
TGGTGGAGAC	
GATAACCTTGT	
TCGCTAAAGT	
TGAAGGCGTA	
GTACGCTTGT	
ACGTAAGGAG	
ACG	

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CTGGATAATT GGAGCAATT C	TGATGCCAG TTTGAGGTTA CTGATAGGAT TGTGGCGAT	60
AGCCACTTGA GAAGATGCCA AGAGTCAT T	TCTCTCTCG TTTAATTGCA CCCCGTGAGC	120
AAATACGGAC GGATGATCTA AATAACCCAG TTCTTCAGA AAAGCAAGGG GGCCTTTGCC	180	
GTACCGTTG AGGATAATT C	TGACTCCTC CTTGGTCTCC GCCACATGGA CATGGAGCGG	240
AATATTTAGC TCTTTGCCA TTTCAGA CGCTTCCAGC AAGTCTCTAC TGCAGCTATA	300	
CGGAGAATGA GGTGCTACCA TAACCCCTGA AATTGGGAT TTTTATATTT TAAGATTTCG	360	
TCTATGATGG ATCGAGTTCT GCTTATAGTC TCAGCAGTTG TTTCTGTCTC TGAAGAAAAG	420	
AGAGTCGGAG AAAAATAACA ACGCATCTG GAAGTTTCA CCACCTGATA AATTGCTGG	480	
ATATCCACAC CATGGGATT ATACATATCG TTAAAGGTTG TTGTTCCCTGA CTGGAGCATC	540	
TCTGTTAGGG CTTCTTGAC CGCATTGGTA GTCATGTCGG GAGTAAACTC AGATTCTGCT	600	
GGCCAGATAT AGTCATTGAG CCATTTCATG GAGATTGCTG TCATCTCGGA TCCCTCTCAG	660	
ACCTGTCATT GCAGATGGG TGTGACAATT GACCAAAACCA GGCATAAGCC AAG	713	

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

CTAGAAAATC TGCTTTTTTC TCGAAAAGTT TAATACTTGG TACAATATTA CGCTTGCTTT	60
GCTCGGCTGC TCCAAGGGCA ATTTCCTCA GTTTTCAAC TTTTTACCC AATTTCCTTGC	120
CATCCCACCTT GGCAACTGAC CAGTCTGCAG GAAAGGCCA GATTGGCTA GCACCCAGTT	180
CGGTTACTTT TTGAGCGATG AACTCCAGCT TGTCTCCCTT GGGAAATCCA GATGCGATGG	240
TCACCTGGAC TGGTAGTTCC ACATTGTCA TTAATTCTTG GACCAACTCA AACTGACGAT	300
TTTCCATATC CAGCACCGCGC GCCAAGCGCT TGATGCCATC ATCAAAGACT AAGGTAACCT	360
CATCCTCTTC TTTCAAGCGC ATAACCTGAA ACATATGCTT ACTGGTTTCC TTGTCCTCGA	420
TAGTGACAGG AGAGATAGCA CTGCCTTTA CAAAATACTG CTGCATGCTA GCCTCCAATC	480
ACACCAGAGA TATCCTGGT TTTCTTAAAG ACACAGGTAT TCCATTCCCC TTGAACCATG	540
TGAGTTTCA GGAAAATCC AGCTGATTCA GCCGACTCGC GCACCATGTC CCACCTTATGC	600
CTTGAATAAT GCCACTCATG ATCAGGTAGC CTTCGTCTT AACCAAACGA TAGGCATCGT	660
CTATTAGATG AATGAGGATA TCCGCCAAGA TATTAGCCAC AATCACATCT GCCTCAATT	720
CCACACCCCTT AAGCAAATCT CCAGCCGCTA CATGGATATT TTCCATGCCA GGGTTGAG	778

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CTTCCCAGAT	TTTTTCGTTG	ACTTGCTGTT	CAATCGCACG	CAATTCTCA	GCAGTTACAG	60
CTTGGAAAGTG	GGTAAAGTCA	AAGCGAAGGA	ATTCAACTTC	GTTAAGAGAT	CCTGCCTGTG	120
TTGCGTGGTT	TCCAAGGATA	TTGTGAAGGG	CAGCGTGAAG	CAAATGAGTC	GCAGTGTGGT	180
TTTTCATGAC	ACGGTGACGG	CGATTGCTAT	CAATTGCCAA	GGTATATTCT	TGGTTCAAGG	240
CAAGCGGTGC	AAGGACTTCA	ACTGTATGAA	GGGCTTGACC	ATTTGGGCT	TTCTGAACAT	300
TGGTCACAGT	AGCCACAACC	TTACCTGACT	CATCCAAGAT	TTGTCCGTAG	TCAGCTACCT	360
GTCCACCCAT	TTCAGCATAA	AATGACGTTT	CCCGCAAAGA	TAAGAGAGGC	AGTTCCCTCT	420
GAAACAGCTT	CTACTTCCTGC	ATTGTCGGCC	ACGAATAGCT	ACCAATTAG	AAGACAATTG	480
GCTAGCATTG	TAGTTGAAGG	CACTTTCTAC	AGTGTATGTTT	TGAAGAGTTT	CCATTTGCA	540
TACCCATTGA	GCCACCCCTTG	ACAGCTGACG	CACGCGCGCG	TTCTTGTGTT	TCTTCATGG	600
CTGCTTCAAA	ACCTTCACGG	TCTACAGTCA	TACCAAGCTTC	TTCAGCGATT	TCTTCAGTCA	660
ATTCAACTGG	GAACCCATAA	GTATCATAGA	GTTTGAAGAC	ATCTGAACCA	GCGATAACAG	720
ATTGACCTTT	TTCTTTCAAG	TCTGCTACAA	TGCCTTGGGC	AAAGTGTGTA	CCTTGAGTGA	780
AGGGTACGGG	CAAATGATTC	TTCTTCGCT	CTTAACGATT	TTCTCAATAA	AGTCACGTTT	840
CTCAAGCACT	TCTGGGTAGT	AGCTTTCCAT	GATTTTCCA	ACAGTTGAA	CGAGTTTTGT	900
AAAGGAAAGG	CTCGTTGATA	CCCAATTGTTT	GACCCATGCA	TAGAAGCACG	ACGGAGAAGA	960
CGACGAAAGG	ACATAACCAC	GACCCCTCCAT	TTCCTGGAAG	GGCACCATCC	ACCGATGGCA	1020
AATGAAAGTG	AACGGATGTT	GGTCCCGCAA	TGAACCTTGAA	AT		1062

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 865 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CTCAAAGTC GCACCTGCAA TACGACCCGC TACAGGACCT ACACTTGCTC CATGCTTGGG	60
ACTATTGCT ACATAACTAC CAAAGTCATC AAATCCAAG ATAACATTGG CAAAATTTC	120
AGCCTTGCA GGTGCGACAT AGCGCAAGAT AGTCGCACCA TAAGTCATAA CCTCAAGMTG	180
GTAGCCACCG TCTGTCTCAA ATCGATAGGC CAAGACATCC TCACCCCTCAA CATTTC	240
TACACGCTCT GTGTATGCTT TCATTCTGTT CTCCCTTAC TATTCTCTC AAGCAAACAA	300
ACCATAGAAA GCGTACTGAC AATCTATGGT TTATCTGATA ATTACAAAT CCTCTTGTC	360
AGAATTCTATA AACACTGTCT TACTTTGAT ATTCTGAAT TATGACACCT TGTACTACAC	420
GGTTTACTGT ACCTGTAGGA GACGGTGTAT CTGGTTTATT TTCTACCTTG AGTGAAGTC	480
ATAGGGCAAA GAGTTGGCA TAAACGATGT AAGGGAAGAC ACGGTAATA TCATTCAAGA	540
CACCGCCACA ACCAAGGGCC ACTTCTTGA CATTTCAG ACCAAAAGCT TGATCACTCA	600
AAAGCACAAC ACGACGAGCA ATCTGGTCAC CAGCAACTTC ACGAACCAAG TCCAAGTCGT	660
ACTTACGAGT GTAGTCCGTC CTTGTACCAA AGAACAAA AACTGTATTG TCGTTGATAA	720
GATATTGGA CGGTGACGGA ACCAACTGGG CTTTCATACA TGGTCGCAAC TTGAACAACA	780
GTAAATCCA AATCTTGAGC TGAGCCTCAT GAGCAGTCCA AAGAAGACCA GCGCCTAGAA	840
GAGACCGGTT AAGTCTTAAT CACAG	865

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 946 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TTTGCTCCA GTTGATAAGA AAGGCTTGGT CGATGTTGAG GCGTTAGCAG GTTTGATACC	60
GCCTGATACA ATCCTCGTT CCCATCATGG CTGTGAACAA TGAAATCGGC TCTATCCAAC	120
CNATTGAGGC TATTTCAGAA TTCTTGGCAG ACAAGCCGAC TATTTCTTC CACGTTGATG	180
CGGTTCAAGGC GCTTGCCAAA ATTCCGACTG AAAAGTATCT GACAGAACGG GTGGATTGCG	240
CGACCTTCTC GAGTCATAAA TTTCATGGTG TCCGTTGGT TGGCTTGTC TATATCAAAT	300
CTGGCAAGAAA GATTACACCT CTTCTTACAG GTGGTGGCCA GGAGCAGAGAT TATCGTTGCA	360
CAACTGAAAA TGTGGCAGGG ATTGCAGCGA CAGCCAAGGC TCTCCGTTA TCTATGGAAA	420
AGCTAGATAT CTTTAGGAGC AAGACTGGGC AGATGAAGGC AGTGAATTCAC CAAGCTCTTC	480
TGAACATATCC GGATATTTT GTCTTTTCAAG ATGAGGAAGA CTTTGCACCT CATATTCTGA	540
CTTTTGAAT CAAAGGTGTT CGAGGTGAAG TCATCGTCA CGCCTTGAA GACTATGATA	600
TTTCATCTC AACAAACCTCA GCTTGTTCAT CTAAGGCAGG AAAACAGCC GGTACCTTGA	660
TTGCCATGGG AGTGGACAAA GATAAGGCCA AGTCAGCTGT GCGTCTTAGC CTAGACTTGG	720
AAAATGATAT GAGTCAGGTC GAGCAGTTTGACCAAGTT AAAATTGATT TACAATCAA	780
CTAGAAAAGT AAGATAGGAG CATTCTATGCA GTATTCAAGA ATTATGATTG CGTACGGAGA	840
GTGTCAACC AAGGGTTAAA AACCGTATGC GTTTCATCAA TAAACTTCGT AATAATATTT	900
CGGACGTTTT GTCTATCTAT ACCCAAGTTA AGGTAACAGC AGATCG	946

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CTTGCTCGTA ACAGGTGCTA TCCTTGGTGT CAATGTTAAC	60
CTTCCCAGAA AAAGAAATCG TTGAATTGGC AGAAGGATTG GCTAAAGAAA GTGGCGCACA	120
TGTTCTCATC ACTGAAGATG CTGATGAACG AGTTAAAGAT GCAGACGTTTC TTTACACAGA	180
CGTTTGGGTA TCAATGGGTG AAGAAGACAA ATTGCGAGAA CGTGTAGCTC TTCTTAAACC	240
TTACCAAGTC AATATGGACT TAGTTAAAAA AGCAGGCAAT GAAAACTTGA TCTTCCTACA	300
CTGCTTGCCA GCATTCCACG ATACTCACAC TGTTTATGGT AAAGACGTTG CTGAAAAATT	360
TGGTGTAGAA GAAATGGAAG TAACAGACGA AGTCTTCCGC AGCAAGTACG CTCGCCACTT	420
CGATCAAGCA GAAAACCGTA TGCACACTAT CAAAGCTGTT ATGGCTGCTA CACTTGGTAA	480
CCTTTATATT CCTAAAGTAT AATTTTAGAT AATAAACCGT CTACCAACAG CTATGAGGGC	540
TGCGACTAAT AG	552

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CTAAAAAAAG TCAAGTAGAA AACGAATATT CTACTTAAC TGCACCAAAT TATTTTTCAC	60
GAATGACTTC GACCTTATAT CCATCAGGGT CTTTGACAAA GTAATAGTTT GGTGCAGTT	120
CTGGTAGACC ATTTGGCTCA GTCACTTCAT AGCCTTTGT ACTGTGCTCT TGATGAAGTG	180
CCTCAAGATC AGGTGTACTG AGGGCGATAT CGGCAAACCC ATCACCAACC ACATACGGAC	240
CGTGATCGTA GTTATAAGTC AACTCCAAT CATACTCATC ACCCTCAAGA CCTAGATAGA	300
CAATCGTGAA GGCATGGTCT GGAAAATCTC TGCGACGCAA TTCTTTAAAA CCAAAAGCAT	360
CTTGATAAAA TGCAATTGAT TTTCAAGAT TTTCTACTCG TAAGCAAGTG TGTAGCATT	420
TTGAAGCCAT ATCCTTCTCC TTATTTTTA AAAAGACTGG ACAATCCTGT TCCAGTCTCA	480

TCAGTTGTTA TTTACCAAGT TTTGCTTAG CT

512

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CTGGACCACA CTATTTCTG TGGTGGCTAT CGTGTATGC AAAAGGATCT AGAAGGGACG	60
CTGGATGCTG AAAAACCTCAA GGCTGCTGGT GTTCCGTCG GCCCCCTTTT TGGTAAAATC	120
AAAAACGGCC AGGATCTTGT TTTGGAAGAC GGAACTGAAA TCAAGGCAGC AGACTATATC	180
TCAGCGCAC GTCCAGGTA GATTATCACT ATTTTAGGAG ACACCTGAAA AACGGATGCC	240
AGTGTGCGTC TGGCTGTCAA TGCAAGATGTC CTAGTTCATG AGTCCACTTA TGCAAGGGT	300
GATGAAAAAA TTGCTCGTAA CCATGGTCAC TCAACTAATA TGCAAGCTGC ACAAGTAGCG	360
GTAGAAGCAG GTGCCAAACG CCTCCTACTC ACCATATCA GTGCCGTTT CCTCTCAAAA	420
GATATAAGCA AACTCAAGAA GGACGCTGCC ACAATTGGT AAAATGTCCA TGTGGTCAAA	480
GACTTGGAAA AAATGGAAAT CTACCAAGTCA CAGAAAGGAT AAGTATGCC ACTATTCTCC	540
ATTAACCGGA A	551

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CCGTCATTAT ACCTTTGTCT ATGAAAATGA AGACCTAGTC TATGAGGAGG AAGTCTTATG	60
ATACAGCCAG CAAGTTAGA AGAATTAGCA TCTTTAGTGG AAAAACGGGG CAAGAAGGTC	120
TTCCCTTTTG TGGCAGACTG GTGTGGCGAT TGTCGTTATA TTTATCCTGC CTTACCAAGAG	180
ATTGAGGAGA CCAATCCAGA GTTCACCTTT ATTCAATGG ACCGAGATCA GTATATGGAT	240
TTGGCCAAAC TCTGGGATGT TTACGAATT CCTAGCCTTG TTGTTCTAGA AAAGGACAAG	300
GAAATTGGTC GTTTGTCAA TCGCGACCCTT AAAAGTAAGG AGCAAATTAA CGATTTTTA	360
GCAGGATTGA AATAGGAGAA AAAGGAAACA ATGATTTTA CGTATAACAA AGAACATGTC	420

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GGTGTGTC	TTATGGTCAT	CGTAAAAAAT	AGCGGAGATG	CCAAACTGAA	TGTGGAACGC	480
AAAGGCAAGG	TAGCCCGTGT	TTTCCTCAA	GAAAATGGGG	AAACAGTAG		529

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CTAGGATAGA	CCGCTTTTA	GCATTTATCT	AAGCATTCCA	GAGTACATGT	ATCTTGCATG	60
TGCTCTTCT	TTTGGGTTG	AAACGATAGG	AGAAGGAAAT	CTTAGAATTG	CTTAAATCAA	120
TCGATGCTT	TGCTTGGGA	CCGCCCTCT	TGATTTATTG	GTCGGAACAG	GGATTACCT	180
AACCATGCGG	CTAGGACTCT	TGCAGGTTT	GGCTCTGCC	AAGGCCTTTC	AGCTTATTTT	240
TATCCAGGAT	AAGGGACATG	GTGATGTATC	CAGTTTTACA	GCTCTTGTG	TAACAGGCC	300
TTGGGCATTC	AAACTGGTG	GGAAACAGGG	AAATATCCAT	TAGGGAGTTC	GCGACGGCTA	360
TCAAGGTTGG	TGGACCAGGA	GCTCTATTTT	GGATGTGGAT	GGCGGCTTTC	TTTCCAATGG	420
CTACCAAGTA	TGCGGAAGGA	CTCTTGGCCA	TCAAATACCG	CACCAAGGAC	GACCATGGTG	480
CAGTAGCCGG	AGGTCCCAGT	CATTATATCC	TTCTAGGGAT	GGGAGAAAAG	TGGCGACCAC	540
TTGCTGTTT	TTTGCAAGTA	GCAGGAGTAT	TGGTTGCTCT	CTTGGGAATC	GGAACCTTCA	600
CCCAAGTCAA	CTCGATTACA	GAATCTATCC	AAAATACAAC	GACGATTTCG	CCAGCCATCA	660
CAG						663

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 727 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CCTTGACAC	CAATTCTTCA	CCCGATATGA	TGCGCCCTGC	TCGCTGAGCA	AGCCCCAAGA	60
GATTACTTAT	CTTTTGCTTA	TTCAAGTCCC	AACTCTCTTC	TTTTCACTTT	GTGATCCACA	120
TAAGCGATCA	ACTCGTCATA	AAAGCTTTCT	TCCACTTCCA	TGCTAAAGCT	GGGGTTAAAG	180
ACCTTCTTCT	TTTTCGCCCTC	TAGGGCTTCT	GCATTGTCTA	GTGGATATA	AGCGCCCGGG	240

CCATTGGCCT	TGCCCGTAGG	ATCAATAAAG	ACTTGTCTT	CCTTGTCTT	GACAATGCGG	300
AGCAAATCAC	GCTTATCAAT	CACTTCGTTA	GACACAACAG	ACTTGCAGA	AGGGATTTTT	360
CTTGTTTCA	TCTTCCCTC	CTCTAGCAGC	TTTTATTCTT	CTACAGTATC	GTPTTCTACT	420
TCCAACCTCA	CTGAAGCAGC	GTCTTCCATG	GCTTCAAATT	CGCTAGCAGA	CTTGATATCG	480
ATACGGTAAC	CAGTCAAGTG	AGCCGCCAAG	CGCACGTTT	GTCCACGACG	ACCAATGCCA	540
AGAGAAAGCT	TGTTATCTGG	AACAACCACC	AAGGCACGTT	TGCTGTCGTT	TTCATCAAAG	600
ATAACTTGGT	CAACCTCAGC	AGGAGCGATG	GCATMTGAGA	TAAATTCAAG	TGGATCTGCT	660
ACCCACTCGA	TAACATCGAT	ATTTCCTTCG	ATTGGTACCA	TGCGTCATT	TTTAGCATCG	720
TAACGAG						727

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CTAATGTAAA	TCTATGGGAT	AAACGTTAGC	TTCTTTTAAT	AGATTATTAA	GCAATTTTT	60
AAAACAACTC	ATCAAACAAA	CTCAACTGGT	TATCTCTGGC	ATATTTCAA	GAATAACCCAT	120
CTCATCCATC	TTTCAACCCA	AGGTTGATGA	GAGTCCACCA	CGCTTGCCTA	GTTCCTGTTT	180
AGAGAGGAAT	TCTCCCTCTT	CACCGCGCCCG	CACCAAGTTGC	TTGGCAACGT	TCTCCCCCAG	240
ACCATCCATT	GCTACAAATG	GTGGGATAAG	GGTATCCCCG	TCGATGAGGA	ACTCTGTCGT	300
CTGACTACAG	TAGAGATCTA	ATTACCAAA	CTTGAAACCT	CGTTCCCACA	TCTCATTGAC	360
AATCTCAAGA	GTTGTATAGA	GATCGATTTC	CACATTAGAG	GCTTCATTGT	TCTTCCGTTT	420
TTCAAGGATT	TCTTCCATTTC	TGCGCTTGAT	GACCTCCAAG	CCCGCACCCA	TGGTCTTGAT	480
ATCAAAAGCC	TTAGCACGAA	TGGAGAAGTA	AGCACAGTAG	TAATAAAATAG	GATGGTGAAC	540
CTTGAAGTAA	GCTACACGCA	AGG				563

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 647 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CTAACTTCAA AAGCTTTAG AATATCTTCT TGACTAATCA TATGATTACC GCCCAAGGTT	60
AAGTTTCCA AAATAGAGCC ATTAAGATA TAGGCTTGT GGGTAGGTA ATTAATATGA	120
CGGCGAAGA CTTTTTTAT CAATGTTTT AATATCCTGA TGATTGATGG AAATATGCC	180
TTTGTAGGGT TCAAAGAAAT TGACAATCAT TTTGGCTAAA GTGTTTAC CAGAACACT	240
AACTCCAAC T AGGCTAACCT TATCTCCTTG TTTAACCGTG AGATTAATAT CTGTTAAGGT	300
ATCTCGTCCA AAACCATACT TATAAGAAAG GTCATCAAAT TCAATATCGC CCATCAAAAA	360
ATGTGAATGA ACAGGGTTT CTTGAACCTTG AAATTCAGAT TCGACTAGAT AGACTTCGTT	420
CAAACGGTTA TTAGCGACCT TCGCAGATTG GAGTTGGTT TGGAGGTTGA TAATATTTTC	480
CATAGGAGTT GTAAAGTAAG AAAGAAGTGT GTTAAAGGTA ATCAGCTGAC CGATAGAAAT	540
TTTACTCGAC ATGACTAATT GAGCGCCAAA CCATAGGATA AGGATATTCA GAACTAATT	600
TGTTTCCCCCT GCTTTAAACT CGTTGTAAA ATAGAATATT TACTGAG	647

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CTATCCTNGA ACCAATGATG CTTGTAACAA TCACTGTTCC AGAAGAAAAC CTTGGTGATG	60
TTATGGGTCA CGTAACTGCT CGTCGTGGAC GTGTAGATGG TATGGAAGCA CACGGTAACA	120
GCCAAATCGT TCGTGCTTAC GTTCCACTTG CTGAAATGTT CGGTTACGCA ACAGTTCTTC	180
GTTCTGCATC TCAAGGACGT GGTACATTCA TGATGGTATT TGACCACTAC GAAGATGTAC	240
CTAAGTCAGT ACAAGAAGAA ATTATTAAGA AAAATAAAGG TGAAGACTAA TCCGTCTCA	300
CTCTAGAAGG AAGTCACTTA GTGGCTTCCT TTTGTCTTAA GAAAATACCT CTAATATGG	360
AAAAATAGTA GAAGAATAAT GTGAGGAAAA TGAATGTCAA ATAGTTTGATG AATTTTGATG	420
AATCAATTGG GGATGCTGC TGAAATGAGA CAGGCTCTG CTTTAGCACA GGCTAATATT	480
GAGCGAGTTG TGGTTCATAA AATTAGTAAG GTATGGGAGT TTCATTCCG TATTTCTAA	540
TATTTACCTA TTGAAATCCT TTTACAATT AAAGAAAGTT TGAGCGAAGA ATTTCCNAG	600
AANGCCATCA	610

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TATAAGCATA	GTACCAAGTTG	CCATTGACCT	GGAACCAACT	GTCTTCATAT	CTCCATTACT	60
GCATTTAGGT	AGTACCCAAGT	TGAACCATCT	TGATACCAAC	CAGTTGCCAT	TGCTCCTGAT	120
GAACGGAGAT	AGTACCATTT	GTTCAGG	TTTGCCAAAC	CTGTTTCAT	ATCGCCATTT	180
GGCTGGTCTA	AATAATACCA	AGTGGTACCT	TCCTGATACC	AACCAGTTGC	CATTGCTCCT	240
GATGAACGGA	GATAGTACCA	TTTGTTCAGG	AGGTTTGCC	AACCTGTTTT	CATATGCCA	300
TTTGGCTGGT	CTAAATAATA	CCAAGTGGTA	CCTTCCTGAT	ACCAGCCAGT	GGCCATTGCT	360
CCTGAGGAAC	GGAGGTAGTA	CCACTTATT	CCTAGATATT	GCCAACCTGT	TTGCATAATA	420
CCAGTTGTTG	GATCTAAATA	GTACCAAGTC	AAATCATCGT	TTATCCACCC	CGCACGTCTT	480
TCACCACCAA	GGTAGTTTC	TCCATTAAATT	TCCGTCTTAG	CTAGATAATA	CCAGTAGACT	540
GATCATAAAG	CCAACCTGTC	TCTAAAGAAT	GATTTTGATT	AAAGTAATAG	TTCGTATAAT	600
AACGNTTCTC	TTCTTTATCT	TCTGAATCTT	CACGTTTTC	CCCGTACTTT	CTTCCAACAC	660
TGTCTTTAGT	TTTAATCTCT	AATGTTTCC	AACCAACAAA	CTCTTGTAGC	ACTCCATT	720
TATCGAAGTA	GTACCACTCT	GAATTTGGAA	AACCTTCTAA	TCTCATACCA	TTTGGGTAAG	780
GACCAATTGT	ACTACCTTTA	GATGGAAACG	GGATATATTG	CCAGCCGACA	ACCATCTCTC	840
CAGATAGAGA	ATCAAAATAAA	TAGTACTTAC	CATCAATCAC	TCGCCAGTAG	GTTCCTTGA	900
GGTCCCCCTT	TTTGTAAATAG	GTTCTACCGT	TTTCTTGGAC	AAACTGCCAT	CCTTCAGAGT	960
TATCTGCAAA	TACTGTATTC	GTAG				984

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 842 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CCTCGTTATG	CAGATGAACG	TTATTTCTTG	TCAAAGAGTC	ACAAGAATT	TGTTGATCGT	60
AATCTTTTTA	TTACCAATTG	TGACAAGGAA	ACCACCTGTA	TCAAGCCTTA	TCAGCAGGAT	120
TTGGATTTGC	CACATGGTCT	GGCCTTGGAT	TTTTGCGCTT	TGGATTATTA	TCCGAAAAAT	180
CCAGCTGAGC	GGAAAAAACN	GGTCGTTGA	GCCTTGATTT	ATTCACTCTT	TTGTGCGCAA	240
ACTATTCCAG	AAAAGCATGG	TGCTCTCATG	AAATGGGGAA	GTCGCATT	ACTGGGTTG	300

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ACTCCAAAAT	CTCTCCGTTA	TCGCATCTGG	AAAAAAGCTG	AGAAAGAAAT	GACTAAGTAT	360
GATTGGCTG	ATTGTGATGG	CATTACAGAA	TTATGCTCAG	GTCCTGGCTA	CATGAGAAAC	420
AAGTACCCAA	TCACATCTT	TGAAGACAAT	CTTTCTTGC	CATTGAAGG	AACAGAGATG	480
CCTATTCCAA	TCGGCTATGA	TGTCTATCTC	AGAACTGCTT	TTGGGGATTA	TATGACGCCT	540
CCACCAAGCAG	ACAAGCAGGT	ACCGCATCAG	GATGCTGTCA	TCGCTGATAT	GGATAAGTCT	600
TATACAGAAAT	ACAAGGGAGA	ATATGGTGGC	TAAGAAAAAA	ATCTTATTTT	TTATGTGGTC	660
TTTTTCTCTT	GGAGGTGGTG	CAGAGAAGAT	TCTATCAACC	ATTGTTCAA	ATCTGGATCC	720
AGAAAAGTAT	GATATTGATA	TTNTTGAAT	GGAGCACTTT	GACAAGGGAT	ATGAATCTGT	780
TCCAAAGCAT	GTACGCATTT	AAAATCCCT	TCAAGATTAT	CGCCAAACCA	GATGGATACG	840
AG						842

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 749 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CTGGCAAATA	CAAGGTGACG	ATCATTGGTA	AATCAGCCCCA	CGGTGCTATG	CCTGCTTCAG	60
GTGTCAATGG	TGCGA	CTTAC	CTAGCCCTCT	TCCTTAGCCA	GTGACTTT	120
CCAAAGAATA	CCTTGACATC	ACTGGTAAAA	TTCTCTTGAA	CGACCATGAG	GGTGAAGTC	180
TCAAGATTGC	TCATGTGGAT	AAAAAGATGG	GTGCCCTTC	TATGAATGCA	GGCGTCTTCC	240
GCTTCGATGA	AAACAAGTGCT	GATAATACCA	TTGCCCTCAA	CATCCGCTAT	CCAAAAGGAA	300
CAAGTCCAGA	ACAAATCAAG	TCAATCCTTG	AAAACTTGCC	AGTTGTTCT	GTTAGCCTGT	360
CTGAACACGG	TCACACGCC	CACTATGTTG	CCAATGGAAG	AATCCACTTG	GTTGCAAACC	420
TGGTTGAAAT	GTCATGAAA	AACAGACAGG	CCTTAAAGGT	CATGAACAAG	TCATCGGTGG	480
TGGAACCTTT	GGTCGCTTGT	TAGAGCGCGG	AGTTGCCTAT	GGTGTATGT	TCCCAGACTC	540
AATTGATACC	ATGCACCAAG	CCAATGAATT	TATTGCTTGT	GATGATCTCT	TCCGAGCAGC	600
AGCAATTAT	GCGAAGCTA	TTTACGAATT	GATCAAATAA	AACGATAGAA	GTCTGAGATC	660
TTATGCTTGG	ACTTCTTTT	GGAGGGAAAG	TAGATGTCTC	AAATCGAAAG	AATCAAACAG	720
GCTATCATGG	CGGATTCA	GAATGCCAG				749

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

CTGGATGAAT	TGCAGAAGCG	CAACCTACTG	GGATTGTCT	TCCAAGATTT	TCAACTATTT	60
CCTCATCTAT	CAGTTCTGGA	AAATTTGACT	TTATCGCCTG	TGAAGACCAT	GGGAATGAAG	120
CAGGAAGAGG	CTGAGAAGAA	GCGAGTGG	CTCTTGGAAC	AGTTAGGACT	AGGAGGACAC	180
GCAGAGTCCT	ATCCTTCTC	ACTATCTGGT	GGGCAAAGC	AGCGGGTGGC	TTTGGCGCGT	240
GCTATGATGA	TTGACCCAGA	AATCATTGGC	TACGATGAAC	CAACTCTGC	CCTGGATCCA	300
GAATTACGTT	TGGAAGTGG	GAAGCTAATC	TTGAAAATA	GGGAACCTGG	GATGACCCAC	360
ATTGTGGTTA	CCCATGATT	GCAGTTGGC	TGAAAATATC	GCACATGTTA	TTATTGAAAG	420
TAGAACCTCA	AATAGGAAGA	AAAATGGATT	GAAAAATGG	ATGCTTGAT	TAGTCAGTCT	480
GAAGACTGCC	TTTGTCTTA	GTA				503

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

CTGGAGGGCA	TTCAGTATTA	CTTGAATAGA	GGAAAACATC	ATCTCCCTTA	TGTTCTCAAT	60
ATTGGATTC	CTGGTCAGAA	AAATGACCTC	TTACTCCTTC	GGCTAGATTT	AGCTGGAATT	120
TCAATCTCTA	CTGGCTCAGC	CTGTACTGCA	GGCGTTGTCC	AATCCAGCCA	TGTTCTTAAA	180
GCCATGTATG	GCGCAAATTG	AGAACGCTTG	AAGGAATCCC	TTCGCATCAG	TTTGTGCCA	240
CAAATACCG	TTGAAGACCT	ACAAACCCCTC	GCAAAACCT	TAAAAGAAAT	TATCGGAGGT	300
TAGCCATATG	GCATTGAAA	AAATCATTCA	GTTAAAAAT	TGTCGTTACG	ATTACACTCT	360
TAGCCCTTCT	GTTAAAAAT	TCACCCCTCAA	AGATAACACC	TTTTTGAAA	CTAAGGTTGG	420
TAACATGAA	CTGACTCGCC	TTTTGGAAAA	AGTGCCAAAC	AGCGGTGAAG	GCTTCCAAC	480
CAAATCATC	ATTAACAAGG	AACTTACAGG	GGCTAAAATC	AATATCACTG	ACAAGTTGG	540
CCTTCGTCTA	GTTGATATTT	TCAAATCAGA	AGACCACCAT	ATTCACTCAGG	AAAAATTCTA	600
CTTCCTCATG	GATAG					615

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 954 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CTGCAATGGT TAGCGAGGAT GGTGAAATAG AGGAGCCTTA ACTATTTGA GGAATCCAAG	60
CTGACAGGAC TGGTATGTCT GCTCTTGTC TCTGAAGGCA GACTATACCA GCTGGAAGTT	120
TGACAGATGT GGCACGTGAG AATTATTGGA GGCNTTGACN TANTCAGAGG ATTCTCTCTT	180
GATATTGGGT TTGGCAGAGT TGGATAGTGA GTTGGAAAAT TACCAAGCGG TTATTCAAGC	240
CTATGCCAG TTAGATAATC GCTCGATTTA TGAGCAAACG GGCATTCCA CCTATCAACG	300
AATTGGCTTT GCCTATGCTC AGTTAGGGAA ATTTGAAACG GCTACTGAGT TTTTAGAAAA	360
AGCCCTGGAG TTAGAATAACG ATGACTAAC AGCTTTGAG TTGGCCAGTC TTTATTTGA	420
TCAAGAAGAA TATCAAAAAG CCACCCCTCTA CTTTAAGCAG CTTGATACCA TTTCTCCTGA	480
CTTTGAAGGC TATGAGTATG GGTACAGTC GGCTTACAT AAGGAACATC AAGTTCAAGA	540
AGCCCTGCGT ATCGCTAACC AAGGATTAGA GAAAAATCCC TTTGAAACTC GCCTCTTGCT	600
AGCTGCTTC CAATTTCTT ATGAATTGCA TGATGCTAGT GGTGCAGAAA ATTATCTCCT	660
TACTGCAAA GAAGACCGCTG AGGATAACAGA AGAAATCTTG CTTCGTTTAG CCACTATTAA	720
TCTGGAGCAG GAGCGTTATG AGGATATTCT AGACTTGCAG AGTGAGGGAC CAGAAAATCT	780
TTTGACCAAG TGGATGATTG CTCGTTCTTA TCAAGAAATG GACGATTGG ATACTGCTTA	840
TGAGCATTAT CAAGAGTTGA CAGGAGATTG GAAGGACAAT CCAGAATTTC TGGAACACTA	900
TATCTATCTC TTGCGTTGAA TTGGGACATT TTGAAGAACG AAAATCCCAT GCTC	954

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 564 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CTATGAAACA TTTTGATACT ATTGTCATCG GTGGGGGACC TGCTGGTATG ATGGCTACGA	60
TTTCCAGTAG CTTTTATGGA CAGAAAACCC TCCTCATCGA AAAAAATCGG AAACCTGGAA	120
AAAAAATTAGC TGGGACTGGT GGGGGACGTT GCAATGTGAC CAACAATGGT AGCTTAGACAA	180
ACCTGCTAGC TGGAATTCCCT GGAAACGGAC GCTTTCTTTA CAGTGTGTTTC TCCCAGTTCC	240
ATAATCATGA CATCATCAAC TTTTTACAG AAAATGGTGT TAAACTTAAG GTCGAAGACCC	300
ACGGACGCGT CTTTCCAGCC AGTGACAAGT CTCGGACTAT TATCGAAGCT TTGGAAAAGA	360
AAATCACTGA ACTAGGTGGT CAAGTTGCTA CTCCAAATAG AAATCGTTTC TGTTAAAAAA	420
GTAGATGACC AGTTTGTCTT TAAGTCAGCG GATCAAACCT TCACCTGTGA GAAACTCATT	480

GTCACAACAG GTGGTAAGTC TTATCCTTCG ACTGGTTCGA CTGGTTTGG TCACAATGCT	540
CCGCCATTAA AGCATACCAT CACG	564

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CTCCGTGGTC TTTTGGTTTG CTACGGGATG TAGGCAAAAG GCAAGTCCAT TTTATCAGCA	60
ATAATGGCTC CGTGTGGAAT CCCTGCTGTT GCAGTTCCTG CAATCACTTC TACTTCAGGA	120
AAGGCTTCCT TGATAGCTTC CACAAAACCA TTTTCAATTAA GGGTACGAGT TTCTGGATAG	180
GCTAGTGTCA CACGATTATC AGTGTAAATC GGTGACTTGA TACCAGATGC CCAAGTGAAG	240
GGTTCCCTCTG GTTTGAGGTA AACGGCTTGG ATTTTCAAGA GGTGGCTAGC GATATCTTTA	300
GCAAGTGTCA TGGTATTCTC CTTTTATTTT TCTAACCTAG TTCTTTAATT CCAGTCCTGT	360
GTCCATTTCAT CCTTGATGGC ATGATAAGCT GCAACAGGAT CCTCAGCTTG GGTAATGGGA	420
CGTCCCACCA CGATATAGTC ACTGCCGATT TGATAGGCAT CAGCAGGTGT CATGACTCGT	480
TTTTGATCTC CAACTGCAAC ACCAGCTGGA CCAATCCCTG GTGCCCCGAC AGATAAAAAT	540
CTGGATTGGT AGCCCTGCTT GATGACTTTG TCACCTCCCT GAGCCGAGCC AAACCAACAC	600
CCATCCCCAA GCCCAAGCTT CAGCTGTCTT CCTTGGCATA GTTGAATCCA C	651

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 602 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CTTAGTATCT AGAAAAGGAG AAATAAAATG GTTAAAGTAT TAGCAGCGTG CGGAAATGGA	60
ATGGGTTCAT CAATGGTTAT CAAGATGAAG GTTGAATG CTCTCCGTAA GCTTAATCAA	120
ACAGATTTTA CAGTCATTTC ATGCAGTGTG GGTGAAGCTA AAGGTTTAGC AGTAGGATAT	180
GACATCGTAA TCGCTTCTCT TCATTTGATT CAAGAATTGG AAGGGCGAAC TAATGGGAAG	240
TTAATTGGCC TTGATAACTT GATGGATGAT AAAGAAATCA CCGAAAAACT CAGTCAGCA	300

ATACAGTAAA AGGTTGGAGG GGGCTGGACA CAAACTGAGA GTTATCGTTT CTGTCCTTCT	360
CCCTCTTAA ATAAAGGAGG CAGATATGAA TTTAAACAA GCTTTAATTG ACAACGACTC	420
GATCCGACTA GGTTTAGAAG CTAACGAATG GAAAGAAGCA GTCAAGGTAG CAGTAGATCC	480
CTTGATTGAA AGTGGGGCAA TTTGCCAGA GTATTACGAT GCTATCATTG AATCGACTGA	540
AGAGTATGGG CCTTACTATA TCTTGATGCC AGGTATGGCT ATGCCACG CTAGACCTGA	600
AG	602

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ATTGGGAATT TTTGCAACTG CAATTGGTGC CCTCAGTAAT CTATAAAATA GATTCAAGAA	60
AATTTACTGA CTGGGATTTTC CCAGCCCTTT TTTAAAGTGA GAAGAAATAA TGAGTATGTT	120
TTTAGATACA GCTAAAGATTA AGGTCAAGGC TGGTAATGGT GGCGATGGTA TGGTTGCCTT	180
TCGTCGTGAA AAATATGTCC CTAATGGAGG CCCTTGGGGT GGTGATGGTG GTCGTGGAGG	240
CAATGTGGTC TTCGTTGTAG ACGAAGGACT ACGTACCTTG ATGGATTTC GCTACAATCG	300
TCATTTCAAG GCTGATTCTG GTGAAAAAGG GATGACCAAA GGGATGCATG GTCGTGGTGC	360
TGAGGACCTT AGAGTTCGAG TACCACAAGG TACGACTGTT CGTGATGCGG AGACTGGCAA	420
GGTTTTAAC A GATTGATTG AACATGGCA AGAATTATTC GTTGCCCACG GTGGTCCGTG	480
GTGGACGTGG AAATATTCTGT TTCCGACAC CAAAAAATCC TGCACCGGAA ATCTCTGAAA	540
ATGGAGAACC AGGTTCAAGGA ACGTGAGTTT ACAATTGGAA CTTAAA	586

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TTCGACAATC TTGCCCCNGA TCCAAGACAA CCACCTCTCT GTCCGCTCAG CAATAGTCAC	60
CGGGTGAGCA ATGAAAATCA AAGCTCTTGT CCAAAGCCAT GAGATAATGG ACAATCCGTT	120

TTTTGTCAA AATATCCAAA CTGTTAGTCG CCTCATCAA AATCAAGACC GGCGCATCTG	180
TCAAGAGAGC ACGCGCCAAA GCGATTCTCT GACGTTGACC ACCTGAAATC CCTGCCCAT	240
CCGAAGTCAA TTCTGTCTGG TAAATTCAA GGTGGCATGG CGGCTTCGAG ATATTCCTCT	300
TCGGAATCTC TGAACCAAAT TCGGACCGGC CCGTTAAAGA TATCTCCCT GTGTCGTCCC	360
CTCCCTTGGC TCCCCAAAAGA AGAATTCTCCA AAATCGTTCC GTTAAAGACA TAGGGCTGTG	420
GAGGCAGATA GATGATGTAC TGCGTAGGG CTTTTTTATC AATCTGATTG AGATTGACAC	480
CACCCAGACT AATCTCCCT TGACTTGGGT CGTAAAAATT AACCATCATC TTGGCCAAAG	540
TCGTCTTACCC TGACCTGAA ATCCCCACAA AAGCCACCTT AGACCCCTGG GGAACGGTTA	600
AATTGATATC CGACAAGACG TCTCGACCAT AGCCATACTT GTAATGAACC TGCTTGAAAG	660
TCATCTCTCC CTTCATCAAG	680

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

CCAATTGGA TTTGCGAGAA GGCGTTATTA TTTCAGATGC TGGTCGACC AAGTCAACCA	60
TTGTGGATGC GGCGGAGCAG TATTGGCTG GCAAGTCTGT TCGCTTGTC GGGGCCATC	120
CCATGGCTGG TAGTCACAAG ACAGGGCTG CTTCGCAGA TGTCAATCTT TMTGAAAATG	180
CCTATTATAT CTTTACAACC TTCCAAAGCC CTGAACAAGT CAAGGACAAC GCTTAAAGGA	240
AATGGAAAG GATCTGCTT CCAGGTCTTC ATGGCTCGTT TTATCGAGAT TGATGCCAAG	300
GAGCATGATC GTGTCACTTC TCAGATTAGC CATTTCCTC ATATTTGGC TTCTAGTCTC	360
ATGGAGCAGA CTGCGGTCTA TGCTCAAGAG CATGAGAATG GCAAGGCCT TTGCGGCAGG	420
TGGTTTTGCA GATATGACCC GAATTGCGGA AAGCGAGCCA GGAATGTGGA CCTCCATTCT	480
CTTGTCCAAT AGCGAGACCA TTCTGGATAG AATTGAGGAT TTCAAGGAAC GTTTGGAAGC	540
GATTGGTCAG GCCATTAGTA AGGGAGATGA AGAGCAAATT TGGAACTTTT TTAACCAAGC	600
G	601

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CTGGCTCATC AGGGCAGGA TATTATGAT TTCCCTCGTG CTATGATTAA GGAAGATAAT	60
CTGGAGTTTT CATTCTCTGG TTTGAAATCT GCCTTTATCA ATCTTCACCA CAATGCCGAG	120
CAAAAGGGAG AAAGTCTGTC TACAGAGGAT TTGTGTGCTT CCTTCCAAGC AGCTGTACTG	180
GATATTCTCA TGGCAAAAAC CAAGAAGGCT TTGGAGAAAT ATCCTGTTAA AACCTGGTT	240
GTGGCAGGTG GTGTGGCAGC CAATAAAGGT CTCAGAGAAC GCCTAGCAGC CGAGGTTACA	300
GATGTCAAGG TCATCATTC ACCTCTGCAGC CTCTGCGGAG ACAATGCCAGG TATGATTGCT	360
TATGCCAGTG TCAGCGAGTG GAACAAAGAA AACTTTGCAA ACTTGGACCT CAATGCCAAA	420
CCAAGCCTCG CTTTGATAC CATGGAATAA AGAGTGGCTC TTGTCAGT GTAGTGGTA	480
GGCGAAAAGC TACAATCTGG AGANTACGAA ATT	514

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

CTTGGATTAT AAAATACAAT CGGCAAGATC ATAAGTCCC AGCCTAAAAA TATATAGAAA	60
GGGGGTCACC TTCCAAAGAA ATTCTGTATT AAAGAGCATG ACCACAAAAC CAATCACAAG	120
CCCCAAGGCA ATCCAGGCGA CCTGCTGCC TAAAATGGC AGAATATTAT TGGGGTAATC	180
ATGACTAACG GCTATATAGA TAGCCACAC ACCGATGACC AGTAGAAAAA ATACTGGCAA	240
GAGCAAACGT TAATCGACTC TTGAGTCGAG AGAACGTTTC ATATAAACTA ACCTTATACT	300
TTCATACAAT ACTATTATC AAAGTTCATT AAAAAATCTA TCAATAGCCT CGTCAACTTC	360
GGATCGAGAG ATGGTTTTAA CAGTCGCTTC TTCTGCTAGA GATGCTACTA TTGTTTGCC	420
GTATCGTTT CCGACGATTG TCCTATCCAA AATAAGAGTT AAGGAACGTT GGTATTACCG	480
TCTCATACTT CTTCCAAAG CCTGTTTAA ACGAATAATG G	521

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CTTGCCGTGAT GACATCATTG ACTCTTTTG GTATATCATC GACCATTCT TAAAAAATGT	60
CTTGAATG GAAGAAGAAC TCGAGTTCA ATTGCTTAAT AACCAAGGAA AGATTACCTT	120
CCACTTTCA AGTCAACACC TCCCTACAGC CATTGATTT GACTTAACC ATCCTTCGA	180
CCCTCGTTAT CCCCAAGAG TACTGGTTT AGACATGGAC GGTAGAGAAA CTATCCTCCT	240
CCCAGAAGAA AATGACCTAT TTAAAAACT CTAGCCTCA GTTGCAGTG ACTGAAAACT	300
AGAGTTTTTC TATTTTTCA AAGCATATA CAAGTTGCGG ATCGGTTGTT TTAATATCGG	360
ATGGATAAAA TGAGGCGCAA TTTCCTGTA GGACTCAAGG ACAAAAAGGC GTTCCCGCTA	420
TGTTAAGGGA TGAGGCAATA TGAGGTCGTC TGTATAAAGG ATCTGGTCCT CCCACAAAGA	480
GCAAGTCCA AATCAATCCA AACGAAGTCC CCCAATGCAC TTCTCTCACC CGTCCCCAGC	540
TCTTGACTCC AATGGCTAAC AAGGTTTCNT ACAATTCTT GTTGCTGGTA GCCAAGTTC	599

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CTATGGTAA AAAGGATGCC TCTGCTATGC ATGAGATGAG GGCTTCCTTT ATTCAAGGCT	60
CCATAGAACG AGGCCATACT GCGGAAAAT CAGAGCAGGT TTTTGATGTT ATGGAGAAAGT	120
TTGCAGGTTA TGGATTTAAT AGATCTCATG CCTACGCCA CTCAGCCTTG GCCTTCCAGT	180
TGGCTTATTT CAAAACGCAT TATCCAGCCA TTTTTTATCA GGTCACTGTT AATTATTCCA	240
ACAGTGATTA CTTAATAGAT GCACCTGAAG CAGGTTTGA AGTAGCCTCT CTATCCATCA	300
ATACTATTCC CTATCACGAT AAAATTGCCA ACAAGTCTAT CTATATAGGT TTGAAATCGA	360
TTAAGGGCT CCAGCAAGGA CTTGGCGCTT TGGATTATG AACATAGACC TTATTCTAAC	420
ATTGAAGATT TTATAGCTAA ATTACCTGAG AATTATCTGA AACTTCCTCC TGCTAGAAC	480
TTTGGTAAAA GTGGTCTTT TCGATTCTT TGAAAAAAAT CGTCCAAAAG TATTTAATAA	540
CTTAGCTATC TATTGAATTG TGAA	564

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ACTAATCACT TACTACGTAG CTTCTGACTA TCTACCTCTA CTAGATAAAG GACAAACTGT	60
AAGATTAAAA CTGGAGAAGN TTGGAATCA CGGCATTACC ACCATCGGCC AACTTCAGAC	120
AATTGATCAA ACTCCTACCA GAACAGAGCA AGGCAATCTC TTTAAATTAA CCGCTCTTGC	180
AAAACTATCT AATGAGGATA GTAAACTCAT CCAATATGGC TTACAAGGTC GCGTCACTAG	240
TGTAACTGCA AAGAAAACAT ATTTTGATTA TTTCAAAGAT AAAATTAA CCCATTCTGA	300
TTAATTTCATA GATAACACTC TATAACTATT TATTATCTTA TCAAAAAGGA GAATCATAAAC	360
ATGGATAAGA AACAAAACCT AACTTCATTT CAAGAACTAA CAACTACCGA ACTCAACCAA	420
ATTACAGGTG GAGAATGGTG GGAAGAACTC TTACATGAAA CAATTAAAG TAAATTAAAG	480
ATCACAAAAG CACTTGAAC ACCTATTCACT CTATAAAAAC AAGACCGAGA AACAGAACT	540
CTCGGTCTTG TTTTTTATCA TTCTGCATGT ATCACAGTAA GTACCTGACG AAAGACTTGA	600
TTTGGCGAG GTAGTATT	618

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CAGGGGATGC CAGTTGATTT GCTTCAAGTT GACTTGACTC GTACTTGGGA AATCCTCGGA	60
GAAATCACTG GGGATGCTGC TCCAGATGAA CTCATCACCC AACTCTTAG CCAATTCTGT	120
TTAGGAAAAT AAGAAAAATC CATGATCCTT CATTGGTCA TGGATTTAT TGTCTTTATT	180
AGTAATCTGG TCTTAAGACC CCTGTTACAG TTGCTTCTAGT TGCTTCGTAG TCGCCATCTA	240
CGACAACCTT GATAATGCGT TTGACATCTT CTTCTGGTGC TGGAAACAAGA GGTAGACGAG	300
TGGGTCCAGC TTCAAATCCC ATATAGTTAA GAATTGCCTT AACTGGAGCA GGACTTGGAT	360
AAGAGAAGAG AGCATTAAACC TTAGGAATGA ATTACGCTG AATTGCTGCG GCTTTCTTCA	420
TATCGTTTC TGCAATGGCA GTAAACATCT CGTGCATTTC ATCCCCATTT GTATGAGAAG	480
CAACAGAAAT AACCCATCCG CCCCCAAGGTT CATGGCATGG AAAGCATCTC CATCCTCACC	540
TGTATAAAT	549

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

CTGGCTANCA AAATCATACT CATAATCCTT AACACCGACA GAGATAGAAG CAATGAGCCC	60
TTGATCGTGC ATTCGTTAA TAAAAGGAAT GCGTCCTGCC TCATCAAAAC GGTGCATAAG	120
TGTACAAGTA ACCACCTTA GCCAGTTGCT CTGCTACATT TTCATCCAAA ATCGTCTGCA	180
TATTTCGCTGG CACAAACAGGT AGTTTAAAGG TGTGATTCC TAAAGTGACA CTTGTATCCG	240
CTTCTGCACG GCTTTAATG ACACATTTAT TTGGAATCAA TTGAATATCT TCGTAATCAA	300
AAATTGGAAA TTCATTTAAC ATATCGATGT CTCGTTCTT TTGTAATGAC CTACCTATGC	360
TCTCGCATCA CTACGCCCTT TCCGACGTTT CCCTTAAATT TATTATAAAC CAAAAGTACA	420
GTTTTGTCA AATTATTC A TGAAATNAAAT ATATC	455

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 776 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CTCCTGGGTT TTGATTAAC CTAGGGTGC CAAAAAGAGG GTGATGACTT CTTGGACATT	60
CTGGGCTTCC TTGAACAAAT CCTGCAAGCG CAATTGATTT CGTCCAATCA AGGATTCTTT	120
CACAATAATC ATCATGTCCT CAATCTTATA CTCATCCCGC AAGATAGTCG TGTGATTTG	180
TGCAAACCTCC TCTTTTTCT TGGCTAGGAT ATTTGAAAAA GCCAAAAAGA GGTCAATGGT	240
CGTCTTGTCA TGCAACAAGCT CCCCATCTTC GTAAATCAC TCTATCGGCG CTTTGGAAATA	300
ATACTGGGCC CGTTTCTTGG TGCTTGGCTT CCAAGTGCTC ACCCAAGAGC TTGAACCTTGC	360
GATATTCTTC GATTTGAGAG AGGAGGTCCT GCTCCAGGTC ATCCCCAAG TCTGTCACTT	420
CTGCTACCTT CGGAAGGAGT TTACGACTCT TAATCAGCAT GAGCTGACTA GCCATGACCA	480
TGTACTCACC CGTCACTTCC AGACGUATGG CCTGCAGGGT TGAGACATAG GCTAGATACT	540
GTTCGATGAC TTCCGTAATG GGCAACATCGT AGATATCCAT CTGGTACTTA GAAACCAGAT	600
GCAAGAGTAA GTCCAGGGGT CCTTCAAAAT CTTTAATTAA AATATCCATT ATCTATATTT	660
TTCTAAGGTC AGGACTGTTT TTAATCCTAA TTTTTTGGCA ATTCGTACA AATCGACCTT	720
GTTCCTTCTATT TGTCCCTTAGA ATAAACTGTT CACGTAAGAC TTGAGATCGA ATTCT	776

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

ATTGATACCN ATTGTACAGG ACAACTTATT TTGGAGCGCC ATAGCAGGGA TANGGTTAGC	60
AATAGATGCC NTGACCATAG AAACGTTTNT TAGCCAATAC ATAACCTGCT AGAGATGAGG	120
TTGCACAAAC TAAGAACATG GTTACCAATG AGATAAAATAC TGAGTTCCAC ATCCATTGCA	180
AGGCAGGGTT CTGCACCATG AGTTGTTGGA AGTTTTCCAT GGTTGGCATT TTAGGGAAAC	240
ACTGAGGAGG AATAACAATT GTATCAGGTT GTGATTTGAA TGCCCCCTGTC AAAATCCAGT	300
AGAAATGGAAA GATGNACAGC ACAGTCAACA AGAGCAAAAT GATTGTTGAA ATNACAGTAA	360
AGGCTGTTAA TGGTTTTTTT TCTGTAGATT GCATAGCTGT CTCCTTTCTT TAGTATTCTA	420
CGTCGTTCC AAGTACTTTA AATTGAACAA AGCTTACGAT AGCAATCATG ACTGCCAAGA	480
AGACACCAAT TGTGTTGGCA TAGCCGTATT CTGTCATTG GAAGGCTTTT TCGTAAAGGT	540
AGTACATCAA GGTACTTGTT GAGTAGTTTG GACCACCAGA TGTCAAAAGC TGAATCAAGG	600
CGAAACACTG GAATGAGTTA ATTGTTGTGA TGATTGCAAT ATAAAGAGTT GTTGGAAAGAA	660
GGCTTGGCCA TTTAATCTTC CAAAAAACTT GAAACTCAGT TGCACCACATCA ACACG	715

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

CTGGGCTGAG TTTTCCAGAT ACAAAACTG CAACCGAAC TGCAATCCCC CAACCCATAG	60
TAATCACAAT CCAACCTGCA CTGTTGCTCT TGGTTTTGGA AAGAACCAACA CCTGCAACAA	120
CACCAATTCC TAGAAGAACATC AGGATTAAG TCCCTAAAAA TTCTCCAAT ATTCACTCA	180
TCACTTTCTC GTCTCCATTAA AAAAGAAGGG GCGGGCGACA AGGATTGCTA CCCTCCACCT	240
CTTTTATTTT TTCTTAATT TTAAATTCTG CTAAGTCGTT TTGAGCAAGA GCTGCTTTA	300
CATCAGCACG GTAAGTTGCT TTTCTTCTT CTGTCAGTC ATAGAACCGT CCCATTTCAT	360
CCAAAACCTGG CTCAACGATA CTATCCAAGC TATCACGAT AAAGAGCATG TGATTGGTAC	420
GACGAAGAAG GAAGTCAACT GGGCTAAGAG TCAACTCATT GCGCATTGCA TAGTGAAGGG	480

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

CTTAATTATA ACTTAAACAC AAAAGTTTA CACAAACTGT GGATAACTCT TTTGAACTG	60
TGATTTCTT AATGAAATC TATTTTTAT TTGTGAATA AGATGTGAAA AAATAGAGAA	120
TATGTTAGAA TAGAGTCATG AAAATTAAAG TTGTAACAGT TGGAAACTG AAAGAAAAAGT	180
ATTTAAAAGA TGGTATCGCA GAGTATTCAA AACGAATTTC TAGATTTGCT AAGTTGAAA	240
TGATTGAGTT ATCAGATGAA AAAACACCAG ATAAGGCCAG TGAATCAGAA AATCAAAAGA	300
TTTAGAAAT AGAAGGTCAG AGAATTATGAT CAAAAATTGC TGACCGTGAT TTCGTTATTG	360
TGTTAGCCAT TGAAGGGAAA ACTTTCTTCT CAGAAGAATT TAGTAAGCAG TTAGAAGAAA	420
CTTCTATAAA AGGANTTTCT ACTCTTACTT TTATTATTGG GGGAAAGTTA GGATTGTCAT	480
CATCTGTAAA AAATAGAGCC AATCTTCTG TCAGTTTGG TCGCCTAACC TTGCCTCATC	540
AGTTAATGAG ACTAGTTCTT GTTGAACAAA TCTATCGCGC TTTTACGATT CAGCAGGGAT	600
TCCCCTACCA TAAATAGAGA ATTGACTTTT AATTGAATTT TTGGTAGAAT AATTGTGTTA	660
GGTCTCATAG	670

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

CTATAATTAA ATTAGCTGTA TTCCAGTCGT CACGACCAAA CTCTGTTACA GGGACACGAA	60
TGTCAAAACG GTTCTCAATC TCCACAATCA ACTCAACCGT TCCCATACTA TCCAAGACAC	120
CTGCATCAA AAGATCTTCA TCCATCATGT CAGAAACATC TTCCATAAAC AACTCATCAA	180
TAATTTCGAT AACTTCTGAT TTGATATCCA TATTTTATTT CCTTTTATTT TTTAAACCAT	240
AGATTATTCA AGAATCCAGA AAAGATTAAG AATGACAACA TGACAACATG GAAAGTGACA	300

ACCATGCCAA GCAACTGAAT CCAGCGATT TCAGGTAGGG CAGCCTTCCC TGCTTTTTTC	360
CGTTCCCTAT TGAGCGTTTT TTTCTTGCAG ACCCAGGCAT CATTGATGAA CAAGCCTAAG	420
TCCATGAAAG AGTCCCCATAG GCGATATAGT ACCAGGTAC ACCATGCCAA AATCCCCATA	480
ATCCAGCATA TTTACAATGT AAGATC	506

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ATGGTTCGAC CCACAAATAT GTTTTGCAGA TCATTGACCA TTCTATGATT TACGTTGCCA	60
TTGCCGGCTC ATACACGCCCG GTTGCTTGA CTTGATGAA TAACTGGTTT GGCTATCTGA	120
TTATTGTCAT CCAATGGGGA ACCGACCATCT TTGGTATTCT CTATAAAATC TTTGCTAAAA	180
AGGTCAATGA GAAATTAGC CTTGCTCTT ACCTGATTAT GGGCTGGTTG GTTCTGGCTA	240
TCATTCCCTGC CATTATCAGT CAAACNACAC CCGTTTCTG GATTCTCATG GTAACGGCG	300
GACTCTGTTA TACAGTTGGA GCTGATTGAT AGCCTTTATG CATTGAAATT TGACAGTTG	360
ACTTATGAAA ATAAACGAGA GGTTATGGAC TTTATCAAGG CTCGTGTTGA TAAGATGATG	420
GGCTCTACTC CAAAAGATAT CAAGGGAAGC AGTTCTTGCA GGTTCAAACACT TTGTTGTGGC	480
AGATATGTTT GGAAGCAGCA AGTGCCTCG TAGAAGTAAG CAAGGAAGAA GATTTAAC	540
CATCTGTTGA ATCACTTTCT CGTGCTTTA ACCTGGCTGA GAAGGCAGAA GGGGTTGCTA	600
CAGMTGATTC AGCACTATTT GAGAATGACC AAGAAAAAGC TTTGGCAGAA GCAGTAGAAA	660
CACTCGTTTT ATCAGGACCT GCAAGTCAGC AATTGAAACA ACTCTTGCG CTTAGCCCAG	720
TCATTGATGC TTTCTTGAA AATACTATGG TAATGGCTGA AGATCAGGCT GTCCGTCAAA	780
ATCGTTTGGC AATCTTGTC AACTAACCA AGAAAGCAGC TAAGTTGCT TGTTTTAAC	840
AAATTAACAC TAAATAAAAT TTGATAAACG GACTTTATCT TATTACAAAG GAGAAGAAAT	900
GGATCCGAAN ANATTGCTCG T	921

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

CTTGGCAACA GGCTCTTTT GTATTGCGTT TATTAAGAAA AACAAAAAAAC ATCGATATAA	60
CATTTAACTA AAAATTATTG TATGTTATCT CCCTTAATTA GGAATGATAA GGGAAATAACT	120
AGAAAGATTT GTGAATACAA ACTATTTCTG ATATACAAAAA TATACAGTAA TAATGAATGA	180
TGGGAGATGG GATGAAAGAA TTCAATTG AGAGAAAGCA GCGTTTTCT TTGAGGCCAT	240
ATGCAATAGG AGCTTGTTCG GTCTTGCTAG GAACGAGTTT ATTGTTTGCT GGTATGGGTG	300
CTCAGCCTGT ACAGGATACA GAAACGAGTT CAGCACTAAT TTCAAGTCAT TATTTGGATG	360
AGCAGGATTT ATCTGAAAAG CTGAAATCTG AGTTGCAATG GTTGAATTAA GAAAACAAGC	420
TTTGAACTT ATGGGAACAT TAGGTTACTA TGAAGGATTT GTTCCATTATG TTTCAAATCA	480
ATACAAAAC CAAGCTGAAG AAGAAGGCAA ACCGCTATCT GATAAAATATA TTTTCGAAAA	540
ATCTTAAGAA AAACATATGC ACCTTCAAAA A	571

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 611 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GTATCAACTC CAAAGAGCAA GTGACTGTCA AAGTTGTAAC AGATGCGGCC AAGAAGCTCA	60
TGGGTGATAA GATTGCTCGC CAGAAAGAAC GTGGGATTCA GATTGANACC TTGCGNACCA	120
TGATTATNGG GATTCCANAC GNTGGTAAAT CCACTCTGAT GAACCGTTTG GCTGGTAAAA	180
AGATTGCTGT TGTTGAAAC AAGCCAGGGG TCACAAAAGG TCAACAATGG CTAAAACCA	240
ATAAAAGATCT GGAAATACTT GGATACACCG GGGATTCTCT GGCCTATAGT TTGAGGATGA	300
AACTGTTGCA CTTAAGTTGG CATTGACTGG AGCTATCAAG GATCAGTTGC TTCTATGGA	360
TGAGGTTACC ATTTTGGA TCAATTATTT CAAAGAACAT TATCCAGAAA AGCTGGCTGA	420
ACGCTTCAAA CAAATGAAAAA TTGAAGAAGA AGCGCCTGTG ATTATTATGG ATATGACCCG	480
CGCCCTCGGT TTCCGTGATG ACTATGACCG TTTTACAGT CTCTCCGTG AAGGAAGTCC	540
GTGATGGCAG ACTCGGTAAC TATACCTTAG ATACATTGGA AGACCTCGAT GGCNACGATT	600
GAACTAAGTC C	611

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1054 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

TTGCTAAAGC AGCCATGATG ANGGCACTCC ATAAGGATAA GTACCACCAA GCAGCAGCAG	60
ANGACCATAA TCTCCTTTAT GACTTGAACG AGAACGTTCA ATAATAACCTT TTTCTAGTAA	120
GGTTTGATTA ATCACTTTCA TCCTTTTCC CTCTCACTTT TATTATACAA CAAAAAGGAG	180
ACGCAGACCT CCTTTTGAA TCTTATATCT AAAATTTAAT ATTCAATTCT GCCATTTAG	240
ATATAGCTAT AGAAAATACA CTCTATTAAT CGAATGTTTC TCTTATTTTC TATCCAATGT	300
CCGAAGTGCT GCTTGATAAG TTTGCTCCAT CAGCATGGTA ATGGTCATAG GACCGACACC	360
TCCAGGGACT GGCCTGATAT GGCTAGCAAG TGCTGCAACT GCCTCATAAT CAACATCTCC	420
ACAGAGCTTC CCATTTTCAT CTCGGTTCAT CCCAACGTCA ATGACAACCG CACCTGGTTT	480
GACAAAGTCA GCAGTCACAA ACTTGGCGCG GCCGATTGCG ACTACAAGAA TATCTGCTTT	540
AGCAGGCCACC TTGGCAAGAT TATGAGTTCG TGAGTGGGCC AAGGTTACTG TCGCATTTTT	600
AGCCAAAAGA AGCTGAGCCA TAGGTTTCC AACGATATTG GAACGACCGA TTACGACCGC	660
ATTTTACCT TCCAAGTCAA TCCCATATTC ATGAAACATT TCCATAATTCTGCAGGTGT	720
CGAGGGAATC ATGACTGGAT GTCCAGACCA AAGACGTCCC ATGTTTAGGG GATGGAAACC	780
ATCCACATCC TTTTCTGGGT CAATGGCTAA TAAAACCGCC TCTTCATCGA TATGTTTGG	840
TAATGGCAAC TGGACCAAAA TCCCATGCCA AGCTGGATCC CTGATTATAT TTAGCAATCA	900
GGTCTAACAA TTCCTCTTGA GTTAATGGTC TCTGGAACTC GCACTACTTC GCTACGGGAA	960
CCAGCCGCAA GAGCTGACCT CTCCCTGTTG CGAACGTTAA ACTTGGCTGG CTGGATTATC	1020
CCCAACCAAA ATCACTACCA ACCAGGCACT AGAG	1054

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

CTGAACCTGGA TTTTGCTACA AGGTCTGATT TGTCAAAGAG ATGCGAGTTA TGATATGAAG	60
CAGGATGATT TGGATAAGGT AGCAGATTAT CTCTTCAAAA CAGAAGAATG GACCATGTAT	120
GAGTTGATTTC TTTTCCGTAA CCTCTATAGT TTCTACGATG TAGACTATGT CACTCGGATT	180
GGTAGAGAAAG TTATGGAGAG GGAGGAATT TACCAAGAGA TTAGTCGCCA TAAGAGATTA	240
GTGTTGATTTC TGGCCCTCAA TTGTTACCAAG CATTGTTAG AGCATTCTTC TTTTTATAAT	300
GCCAACATT TTGAGGCTTA TACAGAGAAG ATTATTGACA AGGTATTAA GCTTTATGAG	360
CGTAATGTTT TCCATTATTT AAAAGGTTT GCCTTATATC AAAAAGGACA GTGTAAAGAA	420
GGCTGTAAGC AGATGCAAGA GACCATGCAT ATTGTTGATG TGTTAGGTCT TCCAGAGCAA	480

GTTAGCCTAT TATCAGGAAC ACTACGAAAA ATTTGTCAAA AGTTAATTTC CCCAAATAAG	540
GGAAAAAATA AAAAGCTCCT TTGGGTTTG ATACAATAGT TTCAAAATTT GAGAGGAG	598

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

CTACTTCCCG GCCGAGTCGA TTCTCCGCCG ATATCGAGCA TACTGGCTCC TTCTGTTATC	60
AATTTACGAG CCTGCTGGAG CGCCTGCTCA AGAGCAAAA ATTGACCACC GTCCGAAAAG	120
GAGTCTGGGG TTACATTGAT AATTCGCAA ATAGCTGTCT TTGCATGAGT GGCTTTACTG	180
GACATATCGG TCACCCCTC AAGGCTATTTC ATCATATTAT TTCTCTATTT TACCATAAAA	240
AGAAAAAGAT GGACACGATT TCATTCTCATCT TTCTCCAGT AGAAACAAGT AAGCAATTGT	300
CAATAATCTT AAACAGAAAT CCCTAATGTC CGACTCATAA TCACCACAAG AGCCAACAAA	360
CAGAAAGCAA TCCCATTAAAC AATCATGTGA AGTAAGATCG ACATTCCAA ACGTTGGTC	420
TTGTAGGCTG TCCAAGATAG AACTGTGAC ATACCTCCAT AAATCAATAA AGAAGGTAAA	480
TTACTTGGTT GATGTAATAA AGCAAACACA ATCGTACCGA CTACAAAT	528

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

CTATGAGAGA GAATGACCTT CTCTTGATTA CTGGCGACCA TGGAAATGAC CCAACGTATC	60
CAGGAACGGA TCACACTCGG GAATATATTTC CATTGTTGGC CTATAGCCCT GCCTTTAAAG	120
GAAATGGTCT CATTCCAGTA GGACATTTTG CAGATATTTC AGCGACTGTT GCCGATAACT	180
TTGGTGTGGA AACTGCTATG ATTGGGGAAA GTTTCTTAGA TAAATTGGTA TAAGATGACG	240
CGCTATGCTT TGCTGGTGAG AGGTATCAAT GTTGGTGGTA AGAATAAGGT CGTCATGGCG	300
GAGCTTCGTC AAGAATGAC AAACCTGGGA CTGGAAAAG GTGAGAGCT ACATCAATAG	360
TGGCAATATT TTCTTTACT TCGATAGATT CCAAAGCCCC AATTGGTTGA AAAAGCTAGA	420

WO 97/37026

PCT/US97/05306

GACTTTCTT GCAGTCCATT ATCCATTTAT TCCAGAACTT TTTCCCTTAC TGAGTCTAGA	480
GGACTTTGAA GGGCGGAAC TGAAA	505

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

CTATTTCTC ATCTTTTTTA GACTGGTAAT GTATCCCCTA GAGTTTCATT GTTAAGACCT	60
GTCGTATTGA CAACAGTGG A TCCTGATTCC CCATTCCAAG AGTTTTGCC GCATCATATN	120
GACGAAATCT TTTTCTGAGC CAGCAATT TT CTCAGCTAGG GCAATAGCGG CGCTGTTGGC	180
ACTAGATACC AGAGTTGCCT CAAGCAACTC TTCGACAGTA TAATTACGGG CCTCCATAGG	240
AATATTACTG GCTTCAGAAT TTGTCGTCAA TTGATAAGGA TAATCAGAAA TATCTACAGG	300
AGTGGAGAGG GTAATACTTC CGTTTCCAA AGCTTCATAG ACCAGATAAA CAGTAATCAA	360
TTTTGTTATG GAAGCAATT CGACAGGTGG CGTTGCATCC TTCTCATAGA GAATTTCACC	420
AGTATTTGCC TCAACAGCAA TCGCATGTT AGCGGCAATG GTAAAATCTT GAGCAACAGC	480
AGTAGAACCA CCCCTAAAGA GAGAGACAGT TAACAAAGTT AAAAATATTT TTTCATAGT	540
AGTCTTATTC TATCATAAAAG AAAAAAAATA TTCTTGCTTT ATAATTTCAT CTGTTAACGCT	600
TTTGAAAAT ATGGTAAAT AAAGTGAGGG AGGTAACCTCA TGTTTCGTAG AAATAAAATTA	660
TTTTTTGGA CCACAGAAAT TTTACTCTTA ACCATCATCT TTTACCTATG GAGACAGATG	720
GGGTCTTGA TTAACCCCTT TGTTAGCGTG CTTAATACAA TTATGATTCC ATTTCATTTA	780
GGGGGCTTTC TTTATTATTT GACAAAACCT ATTGTTACTT TCTTAAATAA AGTCTGTAAA	840
CTCAATCGTT TGCTTGGTAT TTTAATTACC TTGTGT	876

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

CTTGTCAAAT GCCATGGAAG GGGTTCTTTA CTTCCCTCAA CCAGACTTTT CAAACTGAC	60
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TAGCGCTGAT	CTCCTCTATG	CCTGGGACA	ATCTTCTTT	GCCCTCTCAC	TAGGGGTTAC	120
AGACATGTTG	ACCTATGCTT	CTTACTTGGA	CAAGAAAACC	AATCTAGTCC	AGTCAGGAAT	180
CTCCATCGTA	ACCATGAATA	TCTCGATAGT	CCATCATGGA	AGGTCTAGCC	ATTTTCCCAG	240
CCATGTCAGC	CTTCAATATC	CACTCTGAAA	GGGGACCCAG	CCTGCTCTTT	ATCGTCTTGC	300
CTCAACTCTT	TGACAAGATG	CCTTTGGAA	CCATTTGCTA	CGTCCTCTTC	CTCTTGCAA	360
CTGTCACTTC	TTCTGTCGGT	GATGCTGGAG	ATCAATGTGG	GCAATGTCAC	CAACCAGGAT	420
AACAGCAAAC	GTGCCAAATG	GAGTGTATT	TTAGGAATTT	TGACCTTTGT	CTTGGCATT	480
CCTTCAGCCC	TATCTTACGG	TGTCATGGCG	GATGTTACAA	T		521

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

CTGCAGACAA	TAACTTGGTT	AGCTTAACGG	CTCTTGAGGA	TTCATCCAAG	GATGTAACCT	60
TTACCAAGTTC	GGCTTCAAT	CTAAAAGAAC	GGCGACACCT	TCAAAAAGGG	GATTCCAAGA	120
AAATCCTTAT	CCACGAAGAA	TTGGCTAAGA	AGAACGGTCT	TTCACTTCAT	GACAAGATTG	180
GCTTGGATGC	TGGTCAGTCT	GAATCTGGAA	AAGGACAAAC	AGTAGAGTTT	GAGATTATCG	240
GCATCTTTC	TGGTAAAAAA	CAAGAGAAAT	TCACAGGCTT	GTCTTCTGAC	TTCACTGAAA	300
ATCAAGTCTT	TACAGATTAT	GAAAGTAGCC	AAACCCTTT	GGGCAATAGT	GAAGCTCAAG	360
TCAGTGCAGC	ACGCTTCTAT	GTTAGAAAAT	CCTAAGGAAA	TGGACGGACT	CATGAAGCAG	420
GTAGAAAATC	TGGCCTTGGA	AAATCAAGGC	TACCAAGTCG	AAAAGGAAAA	CAAGGCTTTT	480
GAACAAATCA	AAGACTCAGT	TGCAACTTTC	CAAACCTTCC	TGACCATCTT	CCTTTATGGA	540
TGTTGATAGC	AGA					553

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

CTATGGATGC GGAAGTTCT AAGAACCTTC GCTTGATCCT TGAGCGTAAA GGAATGACCA	60
TCTTGACTGG TACTAAACTG CAAGAAATCA TTGAGGAAAA TGGTCAACTT CGTATCAAGG	120
TTGAAGGAAA AGACAATATC ATCGCAAGCA AAGCTCTCT TTCATTGGGT CGTATGCCAG	180
ACCTTGAAGG TATTGGAGAG GTTGAGTTG ATTGGATCG TGGTTGTATC AAGGTCAATG	240
AATAACATGGA AACTTCAGTT CCACGCATTT ATGCCACCAG GTGACATCAA CGGTACTAAG	300
ATGTTGGCTC ACGCAGCTTT CCGCATGGGT GAAGTTCCG CTGAAAATGC CCTTAAAGGA	360
AATCATGCAG TTGCAAATT GAATTGACT CCTGCAGCCA TCTACACTCT CCCTGAAGTA	420
GCAGCAGTAG GTTTGACAGA AGAACAAAGCC CGTGAGAAAT ACGATGTTGC CATCGTAAG	480
TTTAACCTTG CTGCTAACGG TCGTGTATT GCATCTGACG CAG	523

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

CTGCAGGTGG AATTATGAAT GTCGGATATG AAAAACATT CTTGATGCAG ACATCGTTAA	60
ATTTGCCAAC TTCTGAAATT ATCTCGACAT ATGTCTATAA AGTTGGCTT GTATCAGGAG	120
ACTATTCTTA CTCAACAGCG GTTGGTTGT TTAATGCAGT GATTAACGTA GTATTGCTTG	180
TTGCAGTTAA CCAAATCGTT AAACGCATGA ATAATGGTGA AGGAATTAA GGAGGAAAGT	240
ATGAAAATT CGATTATGGA TACAAATTG GATAGACGTA TCTTACTCTT AAATAAAATC	300
ATTATTGTCT TTATCGTTT GATGACTTTG CTTCCCTTAC TTTATATCGT CGTAGCATCC	360
TTTATGGATC CTAAGGTTCT GGTAGTAGA GGGATTAGCT TTAATCCAGC CGATTGGACT	420
GTAGAAGGTT ACCAGCGTGT TATTCAGTGA CCAATCTATT CTAAGAAGTT TTATCAATTG	480
CCTACTATAC TCTTTGGAT TTGCAGCT	508

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CTAAAAAGAA	CCAGATGGAT	CTTGTGATGA	ATTTACATCA	TMTTGATTTA	CCAGTGGAAC	60	
TTCTTCAAA	AA	ATACGGTGGT	TGGGAAAGCA	AACATGTA	GGAGTTATTC	GTGAAGTTG	120
CCAAGACTGC	TTTCAACATG	CTTGGAGAT	AAGGTTCA	ACTGGACAAC	TTTCAATGAG	180	
CCAATGGTCA	TTCCAGAAGC	AGGATACTTA	TATGCTTCC	ATTATCCAAA	TCTAAAAGGA	240	
AAGGGAAAAG	AGGCCGTACA	AGTCATCTAT	AATCTAAACC	TTGCTAGTGC	AAAAGTGATT	300	
CAACTATATC	GCTCATTAGG	ACTTGATGGA	AAGATTGGA	TTATTTAAA	CTTGACACCT	360	
GCTTATCCAA	GAAGTAATT	TCCAGAAGAC	TTAGAAGCAA	GTGCAATTAC	AGATGACTTC	420	
TTTAACAAAG	TCTTCCTTGA	ATCCAGCTGT	TAAAGGA	ACT TTCCCAGAAA	AGATTGGTAA	480	
AAACAGCTAG	AGAGAGATGG	CGTGTATGG	AGTCATAACCG	AAAAAGAG		528	

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

ACTCTTATTG	GTGAGGTATC	GCAACTTCTG	TTTCTGCCTT	CCTTGGTGG	CCAGCCAATA	60
CAACTTACCG	AGAAAATACA	GGGGTTATCG	GTATGACTCG	TATCGCTTCT	GTCTCAGTTA	120
TCCGTAACGC	TGCCTTCATC	CGCATTGCC	TCAGCTTCCT	TGGTAAATTC	ACTGCCCTG	180
TTTCAACTAT	TCCAAACGCT	GTACTTGGTG	GTATGTCAAT	CCTTCTCTAT	GGGGTTATCG	240
CCAGCAATGG	TTTGAAAGTC	TTGATTAAG	AACGTGTGGA	TTTCGCTCAA	ATGCGAAACC	300
TCATCATCGC	AAAGTGCATG	TTGGTTCTTG	GACTTGGAG	GAGCTATCCT	AAAACTTGGT	360
CCAGTTACAC	TTTCAGGTAC	TGCCCTTCA	GCCATGACAG	GAATCATCTT	GAACATTGATC	420
TTGCCATACG	AAAATAAAGA	CTAAGAGTCT	AAATACACCT	AATCCACTCA	GACAGCTGAG	480
TGGATTTTTC	GTATACCATA	ATAAAAGTGT	CTTAACAAA	TTATTTAAAT	CAAAAAACGT	540
ATAATATCAG	ATATTCTAAA	ACCTTGATAC	TGTACGTTT	ATCATAGAAA	TTTTTACTTT	600
ATTTTCTCAT	CAAATGAGAT	TTGCATCAAT	CTCTTGTCTT	ACTTGCCTT	CTTCTTCGCT	660
TTCTTCATTT	TGTTAGCCAT	ACGTTTCATG	GACTGTTCA	TGGCAAATTC	ACCAATT	720
CCTTTCAAAC	CGCCACCAAA	CATCTGGCTC	ATATCTGGCA	TTCCTGCTCC	TCCGAGAG	778

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GGGAGTTGGT TGCTATTNGT GAGGGAAAAG GTTTGAACCT TGAAATCGAA GTGGATGGTG	60
GGATTGATGA CCAAACATATT GCTCAAGCCA AAGAAGCTGG TGCGACTGTT TTTGTAGCAG	120
GTTCTATGT CTTTAAGGGA GAAGTCATG AGCGAGTACA AACTCTCAGA AAACAACCTGG	180
ACTAGGGTTG CAGTTTTGC AGGCGGAAAC CGCGGTCAATT ATCGGACAGA TTTTGATGCT	240
TTTGTGAGGG TGGATCGAGG CTCGCTCTGG GTCTTGGAAAG AAGACTTACC TCTTGCTCTA	300
GCAGTCGGAG ATTTTGATTC TGTGACGGAA GAAGAGCGAC AGGTGATTCA AAAACGTGCC	360
CAGTATTTTG TCCAAGCCCCG GCCAGAAAAA GATGATACTG ATTTGGAATT GGCTCTCTTA	420
ACCATCTTTG AACAAAATCC TCAGGCTGAG GTCACTATTTC TCGGTGCCCTT GGGTGGCCGT	480
ATTGACCATA TGTTGGCCAA TGTTCTTCT ACCTAGCAAT CCCTAAGTTG GCACCCCTATA	540
TGCCTCNAAGAA TAGAAATTGA GGAATGGCA AATTGATTG CCTATTGTTTC CAGAAGGGAA	600
CAGTCAGATT CGAATCCCTG CA	622

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

CTATTATCAC CACTTTATA CCTATTACCA AAAAAATCCT CAAAATGATT GGCAAAAGGC	60
TTTATCCACC AGCCATTAT CAGCAATATT TACTTGAAA ATATGGTAGA AATAGAAAGG	120
ATGGAGGAAT CTAATGGTAT TACAAAGAAA TGAAATAAT GAAAAGATA CATGGGATCT	180
ATCAACGATC TACCCAAC TG ACCAGGCTTG GGAAGAAGCC TTAAAAGATT TAACAGAAC	240
ATTGGAGACA GTAGCCAGT ATGAAGGCCA TCTCTGGAT AGTGGGATA ACCTACTAGT	300
AAATCACTGA ATTTTCTCTT GAAATGGAAC GCCAGATGGA GAAGCTTAC GTTTATGCTC	360
ATATGAAGAA TGACCAGGAT ACACGTGTAAC GCTAAGTATC AAGAGTACTA TGCCAAGGCC	420
ATGACACTCC TACAGCCAGT TAGACCAAGC CTCTTCATTC TATGATCCTG AATTATGGA	480
TATTAGCGAA AAGCAGT	497

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

CTGTTATGGA GTTGAAAGAA GAATACCACC CAGACGGTAA AGGTTTGAA ATGATCTGTA	60
TCGGTGGGAT GGGAGCTGAT TTCTTTAAGG CTCGCCTGAT TCAACCACTT TATGAATTAC	120
GTGGCTTGTC AGACCAACCT AGCTTTGATC AAGTTCTGAA GATTATTCA AAAACTGTTG	180
AAATGTACCA AAATGAACTC TTTGATGAGC TTTATGTTG CTACAACCAC CATGTCAATA	240
CGCTAACCGAG TCNAATGCGT GTGGAACAAA TGCTTCCGAT TGTTGACTTG GATCCAAATG	300
AAGCGGATGAG AGANTACAGC TTGACTTTTG AAATTGGGAA ACCAGCCGAG AAGAAATTCT	360
GGAGCAGTTG TTGCCTCAGT TTGCAGAAAG TATGATTTAC GGTGCCATT A TCGATGCCAA	420
GACAGCTGAG AATGCTGCGG GTATGACAGC CATGCAAACA GCGACAGATA ATGCTAAGAA	480
AGTCATCAAT GATTGACAA TTCAGTATAA CCGTGCCCAG ACAGGCAGGAT ATTACACAAG	540
AAATTACCGA AATCGTAGCA GTGCCATTATG CCTTAGAATA GCTCTAGTCC CAGCTCTCCT	600
CACTC	605

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

CTACACTTGA GGGAAAGTTG AAAATTCCAT TTTTCTTAAA GGGAAATTGTG AAACGCTATG	60
TATTTTCTTT TTACAACCGG ATGGAGCACT TGGTTGTGGT CAATCCTATG TTTATTGAGG	120
ATTTGGTAGC AGCTGGTATT CCACGTGAAA AAGTGACCTA TATTCTAAC TTTGTCAACA	180
AGGGAAAAAT GGCATCCTCT ACCACAAGAA GAGGTAGTCA GACTGCGCAC AGATCTTGGT	240
CTTAGTGACA ATCAGTTTAT CGTAGTAGGT GCTGGGCAAG TTCAGAAACG TAAAGGGATT	300
GATGACTTTA TCCGTCTGGC TGAGGAATTG CCTCAGATTA CCTTTATCTG GGCTGGTGGC	360
TTCTCTTTTG GTGGTATGAC AGATGGTTAT GAACACTATA AGAAAATTAT GGAAAATCCC	420
CCTAAAATT TGATTTTCC AGGCATTGTA TCGCCAGAGC GGATGCGCGA AATTGTATGC	480
TCTAACGGAT CTTTTCTTGT TGCCATTAA CAATGAG	517

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

TGTTCGCCTC	CATATCCNAA	ACTTGCCCTG	CCACCATAACC	CAGACTACCT	GAAGCAAGGG	60
ATAAGTGGC	AATCGAGCCC	ACCTNGATCT	GACTTGGCGA	ATCTGCCCTGC	GCAATCAAGG	120
CATATGGGT	TAAGAATAAG	GATCTCCAGC	CAAATGGCC	ATAGCTTCAC	CGAATTCTN	180
GTGATTGGTT	AACCGCCCTC	TTCGATAATC	GTCATCATCC	ATAGCAGGAA	GGTCATCGTG	240
AATCAAGCTC	CCTGTATGAA	TCATCTCCAA	GGCAGTAGCT	ACCTGCGCGN	GAGCAGGTTT	300
GATGGTAACC	TGCAAGGCTT	CCAGAACCTTC	TAACAAGAGA	AAAGGCCGAA	TACGCTTGCC	360
ACCAGCATGA	ATAGAATAGA	GAACAGACTC	CCGTAACACTA	GAGGCAAACAT	GCTGGTCTCC	420
ATAAAATCTT	CCAAAGCCGA	CTCGACAAGA	GCTAATTTTT	CTTGCTTTTT	CATTCAAAAT	480
CACTTTCTGT	TCCGTCTTCT	TGCAATGACCT	TGACCAAGGT	CTTTTCAGCC	TTGTCCAGCG	540
TAGCTTGGAG	CTCTTTTGAC	AAGACCATGC	CCCTTTGAAA	GGCAGTAATC	GCATCTTCCA	600
GAGCAATTTC	ACCATTTCC	AAACTTTGGA	CAATGGTTTC	CAGTTCTGCT	AGATTTTCCT	660
CAAATTTCTT	TTGTTTTGAC	ATCTTTAAC	TCTAATTCTA	CTTGACCATC	TCGCATCAAA	720
AGCGTTACTT	GGTCTTTTTT	CTTCAAACTC	TCAACCGAAT	CTACAACGGA	TCTTCTTTTT	780
TGACAATAGC	ATAACCAC					798

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

CCATGTTTGC	GGCAGTGACA	GCAGGTTATC	AGGCTGCCCT	AATGGTACCA	ACAGAAATCC	60
TCGCAGAGCA	ACACTTTGAG	AGTTTACAGA	ACCTTTTCC	CAATTGAAA	CTGGCTCTCT	120
TGACAGGTC	CTTGAAAGCT	GCAGAAAAGA	GAGAAGTCTT	GGAGACCATT	GCCAAGGGTG	180
AGGCTGATTT	GATTATAGGA	ACTCACGCTC	TGATACAAGA	TGGGGTGGAG	TATGCTCGTC	240
TTGGTTTGAT	TATTATCGAT	GAGCAGCAAC	GTGTTGGTGT	AGGGCAAAGG	CGTATTTTAC	300
GGGAAAAAGG	CGACAATCCA	GATGTCCTCA	TGATGACCGC	GACTCCCATT	CCACGGACGC	360
TTGCCATCAC	AGCCTTTGGA	GATATGGATG	TTTCCATAT	CGACCAGATG	CCAGCAGGTC	420
GGAAGCCCTA	TTGTGACGCG	CTGGATCAA	CATGAGCAAC	TACCTCAGGT	CTTGACTTG	480
TTAGAGGGGG	AAATTCAAAA	AGGTTCCCAA	GTCTATGTCA	TCTCTCCTTT	GATTGAAGAA	540

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

CTCTTTAAC CGTMTAGCG GTGACACCGA GGTATTTTT CAGGACCCAA GACTTGTGG	60
GCAACCGAAA CTGGGAGTTTC GTCATCTCCA ATATGCAGAC CAGCAGCATC AACCGCAAGA	120
CAAACATCCA ACCGATCATC GATTATCAAG GGGACCTGAT AGGCATCTGT TATTCCTTG	180
ACTTGTGTTG CCAGTTGATA ATATTGATTCGTTGTGAGAT TTTTTCTCG CAATTGGACT	240
ATGGTAACCC CTGAACGGCA GGCGTCTCA ACTTTGCAA GAAAGCTTC CACGGAATCT	300
TGATAGCGAT TGGTTACCAAG ATATAGTCTA AGCGCTTCTC TATTCTATAAA CCTCTCCTTT	360
GATGGTATCT AGCCAATTTC CATCTCTTCT TAGGAGCGAA AGCTGATTGA GTACTTGGTA	420
ACGAAATTCT TCCAATCCC TTCCCTGAAAC AACTATTTTC TCAGCCAGCG ATATTGAGAT	480
AAGAGACTGC TAAGCAAGAA CTTCAAAACC AGTCTTCCT TGGCTGAGAA AACAG	536

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 854 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

CTGGAGTGAC GATTGAGAAA ATCTTTGCC TAGAAAATTA TCGAAATCAG TTAGCTGCTT	60
TTCCGAAAC TGTCTGGATT TCAGAGGATA TTTTGCTAGA TTTGGCGGAT TCTCAGACTC	120
CACAGGAAAT TGGTGCCTG GTTCAAAAG AAGAAGTAGG ACAAGCTGAT TTGAGTCAGG	180
GCAAGTTCTT GTTTTGAA GATGTGCAAC ATCCTGGTAA TGTAGGAACt ATCATTGAA	240
CTGCGGATGC AGCAGGTTT ACAGGAGTGA TTGTTTCAGA TAAGTCGGCA GACATCTACA	300
GTCTTCAAA CCCTACGTTG CATGCAAGGT AGTCATTTC ATCTGCCAT TTACCGGATG	360
ACTAGTCAAG CGCTTCTTGA CGAAACTAAA AAGGTAGCTA TCCCAGTGCT AGCAACAACC	420
CAATCTAAAG ATTCTGTTGA TTACAGAGAA CTGCCTTCTA TAGAAAATTT TGTACTAGTT	480

ATGGGAAATG AGGGTCAAGG AATTAGTCCC CTTATGGCTG AAAGTGCAGA CCAGTTGGTC	540
CATATTAGCA TGAAGGGCA GGCGAGAGT TTGAATGTTG CGGTTGCAGC CGGTATTTTA	600
ATCTTCCATT TAAGCTAATT TTAACCTTTT TTGTTATAAT CAAGGAAAGA TGTCACAGA	660
AAAGGAGAAA TGGATGAATC ACACTATTAT ACATGACCGT GCAGGTCTCA ATCAATTAA	720
CGCTAAGGTT TATGCCTTG TTGGTCTGGG AATCGGACTA TCTGCTTGG TATCAGGCCT	780
TATGTTGACG GTCTTTCAGT CTCAGTTGGT TTACTTTTG ATGCAGGGC GTCTCTGGTT	840
GACCATTGCT ACTT	854

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

CTGAAGAAAT CCTAAAAGAT TTGTATTACG GAGCCGCTAA GAAAATTCAA GAAGAACGCT	60
CTCGCTGGC AGGAGTTGTA AGAAATGACT AAAACAGCCT TTTTATTGTC TGGTCAAGGT	120
GCCCCAGTATC TACGGATGGG ACGGGATTTC TATGATCAGT ATCCGATTGT CAAAGAAACG	180
ATTGATCGAG CGAGTCAGGT GCTCGGTTAT GATTTACGTT ATCTCATCGA TACGGAAGAA	240
GACAAACTCA ATCAGACCCG CTATACGCAA CCAGCCATTG TAGCGACTTC GGTTGCTATC	300
TACCGTTTAT TGCAAGAAAA GGGCTATCAC CCTGATATGG TTGCTGGTT GTCTCTTGGA	360
GAATACTCTG CCTTGGTGGC AAGCGGCGCC TTGGATTITG AAGATGCCGT TGCCTTGGTA	420
GCTAAGCGTG GAGCCTATAT GGAAGAAGCG GCTCCTGCTG ACTCTGGCAA GATGGTAGCA	480
GTTCTCCATA CCCCGTAGAG TCCTTGAGAA GCCTGTCCAA AGCTCTGACT TGAGTGGTAC	540
TCCAGCCACT ATACACACTG CACAATCTCA TTGCTGGAAA ATTGTTGCAG TGATCAACGG	600
TGACTTTGCA GAGCAGTGCC AACCCCTATCC CCTAGT	636

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CTCTAAAACG AATTCTCTAC AAGCACCGCA AGGGCATGGC TGAACCTCCA CCATAAGGTG	60
GTTTGTCTCG AAAGGCTAAT ACTTCNTTAA CCTTAGTTTG TCCTGAAAAT TGGTACATAT	120
TGAAGAGGGC CGCCCCTCT CGCGAGAGAT GGAAAACACC ACAGGTTCCC TCCATACAGA	180
ATCCTGTAAA TATTTGTCCA TCTCCTGCTT CTACTGCAGC TACAACATGA TTGGCATAAA	240
CAAAGTCTGA TACTTCATGT GGATTGTATA GTTTCTGTGC TTCTTCCTAC ATCTTTTCCC	300
AGATGTCCAT TATTGTATCC TCTATATTAA GAGATTCTT TTAGAATGTT TTCGATATGC	360
TGAATTGATT TTTCACGTCC AAGCAAGAAA ATTGTATCTG GTAATTCTGG CCCATGCATT	420
TCGCCTGAAA CTGCGATACG AATAGGCATG AAAAGATTT TCCCTTAAT ACCTGTTCT	480
TTTTGGACTG CTTTAATTG CGGAAAGATA TTTTCTGTCA CAAATTCAATC ATCTGTCAATC	540
CGCTTCATT TTTGCTTGA ATGCTTCAAG AACTGTTGGA ACTGTTCAC CCGTCATGAC	600
TTCGCGCTCT GCTTCTGTCA ATTCCTGGGA AATCTGAGAA GAAAGATCTG TCCATGGGAT	660
ATCTCATCTA CTGATTCTT GTGGTTTATA GAG	693

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

CTGACAAAGG AGACGGGTAT GGAACAAACA TTCTTTATCA TCAAACCAGA TGGTGTAAAA	60
AGAGGGCTAG TGGGTGAAGT GTTAAAGCGC ATCGAACAC GTGGATTAC AATCGAAAAA	120
TTGGAGTTTC GTTCACAGGT TTTCAGAAGA GTAGATTGAC CAGCACTATC AGGACCTGGT	180
TGGTCAGAGT TTTTACCCAC CGATTCTGTGA ATTCACTGACT TCAGGTCCAG TTCTTGTGGG	240
TGTCATTCTC GGTCCCAAAG TAATCGAAAC TTGGCGGACC ATGATGGGTG CAACTCGTCC	300
AGAAGAAGCT TTACCAAGGCA CTATTCGAGG TGATTTTGCA AAAGCTGCTG GAGAAAATGA	360
GATTATCCAA AATGTTGTAC ATGGTTCAGA TTCCGAGAAG AATCAGCTAA GCCGAGAAAT	420
TGCTCCCTTG GTTTAAGAG TGGATTGGCT CAATCAATTG GATAAAAGCT CATTGAAATA	480
GAAAGTATAG TCAATTAGTT TAAGACATGA CGCATGATAT CAAACTTTT AGTTTTGAT	540
ATGGTGCCTT TTT	553

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

CTAGAGATT	NCGAAGAGTA	TTATTGTACT	TTAAAGGTCT	TGAGATAATT	GTCTTNCCT	60
ACTTGACCTT	CGAAGGTTTT	ACCATTTCA	AGGTAGGAA	GGTCATCGGA	TACTGAAGCC	120
TTGACCTTGT	ATATCTTGCC	ATCAACTTTA	AAGAAGTAGA	CAGTGTCTCC	CTTGATAACA	180
GCTGATTGAA	GGTCTGCTAC	TACTCCCTTG	ATGCTTCTG	TCGTTGCATT	GTCAATTCA	240
AGGTCGTTT	TATTGGCATA	CTTGCTGAGC	ATCTCTTCCA	CTGTAGTAGC	AACGATAACA	300
TTTTGGTACT	CGACTGGCTC	TACCAGGGCG	TACTCTTGA	CCAAGCCAGC	ATTGTCCTTT	360
AAGCCCATGA	TGTAAAGAGG	CTTGTCAATTG	AGGTTGATAA	AGATTGGGA	AAGGTTGCTT	420
TGTAGGATT	CTCCTGAACA	GCACCTCTG	CTGATTCAAG	GGCTGATTCT	TCTGTGCGAG	480
AAGCCAAG						488

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

TACAGCTATC	GGGTCCGTCT	GGTAGTTGGT	CCTCAGAAC	TTCACTGCCA	CTTCTTCCCC	60
ATCTAAGATT	AAGTCTTGG	CTAGGTAGAC	ATCCGCCATG	CCTCCTCGAC	CAATCTGTT	120
GACAATCCGA	TAGCGTCCGG	AAAAAATCTT	GCCGATTGG	ATCATCTTC	ATCCCTCTCG	180
TTCATAGAAA	CAAGGGCAAC	CGTAATGTTG	TCTAAACCTC	CTGCATTGTT	AGCAAAACGA	240
ACAAGTGTCT	CCGTTTATC	TGCTAAAGGA	ATATCACTGG	TTACAATATC	ACGAATCTCA	300
CTGCCTGAAA	TCATGTTGGT	CAAGCCGTCA	CTATTGAGCA	AGAGATAGTC	ACCTGACTCA	360
AGGATAACTG	TCCCCAAATC	AGGCTGAATT	TCATCTTTT	GCCCAATAGA	CTGGGTGATA	420
ATATTTTTT	GTGGATGACT	TCTGCCTCTT	CTGGTGTCAA	TTGACCAGCC	TTGACCAATT	480
CATTAACCAA	AGAATGATCG	CTCGTCAACT	GATGGTATCT	TCTCCACGAA	TCAAGCCGAT	540
ACG						543

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

CTTTAAGGAA AATCAAATCT CTCATGCTGA TACCTCTCCT CATTAATTAA AATAGTAAAA	60
AAGATTCTAT CTCACTCCCT GATTATTACA AAACCATTGA AATATCACAA CTAATAGGCT	120
AGAATGGACA TAGTAAGATN TAGTAGATGA GTCATTCTAC TCAAATCCAC GTTAGAAGAGG	180
ACTGCTATGC CAGACAATCT CGCGCTTCGC ATGCGCCCTA AAACCATCGA CCAGGTCATC	240
GGTCAGGAGC NTCTGGTCGG ACCTGGAAAA ATCATCCGCC GCATGGTGGA AGCCAACCGC	300
CTGTCCTCCA TGATTCTATA TG GCCCTCCT GGAATCGGCA AAACCAAGTAT TGCCCTTGCC	360
ATCGCTGGAA CGACCAAGTA TGCCCTTCGA ACTTTCAATG CGACAGPTGA TAGTTAAAAA	420
GCGACTGCAA GAAATCTCGG AAAAGCTAA ATTTNCTGGT GGTCTCGTCC TATTGCTAGA	480
CGANATTCAT CGACTAGATA GACC	504

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CTAATAGAGG CGAAAAAATT TCAGGTCCCTC CTPTGCTAGA TGATAATGAG GAAACTAAGA	60
TTTTTACCAAC CTCTTCTTCC CGTTTTGGTT ATGCCAATCC TAAGGATCAT GGTTTTAGCC	120
AGGAAACCTT GAAGATTCAAG GTCGAACCAT CTATTCTAA AAGCCGTCGT ATTGAAAATA	180
CCAAGAGAAA TGTCTTCAAT TCTAAGTTGA ATAAAATCTT ATTTGCCGTC ATCTTTCTCT	240
TGATTTTGCT TGTTTTAGCA ATGAAAACCTT TGTAATAGAA AAGGAATTGA AATGAAAATA	300
GGAATTATTG CTGCTATGCC AGAAGAACTG GCTTATCTGG TCCAGCATT AGATAATGCC	360
CAGGAGCAAG TTGTTTGGG GAATACCTAT CATACTGGAA ACCATTGCTT CTCATGAAAG	420
TCGTTCTTGT TAAAAAGTGG AATTGGTAAG GTCATGTCTG CTATGAATTG TGTGGCGAAT	480
TTTGGCTGAT CATTTCAGG TTGGATGCC TTATTAATAC GGGTCAG	528

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CTAATAAGAC TGAAAAGAAG TCCAGCCAGA TGTCCCTAAA AATACAGAAA AAACATTAAA	60
ACCAAAGGAA ATCAAATTAA ATTCTTGGGA AGAATTGTTA AAATGGGAAC CAGGTGCTCG	120
TCAAGATGAT GCTATTAACC CGGGATCTGT TGTCTCGCT TCACGTCGGA CGGTCAATTAA	180
GTCAATGAAA AAGCTACCAA GGAAGCAAAA GTTCAAGCCT TATCAAACAC CAATTCTAAA	240
GCAAAAGACC ATGCTTCGTG TGGTGGAGAA GAGTTCAAGG CCTATGCTTT TGACTATTGG	300
CAATATCTAG ATTCAATGGT CTTCTGGGAA GGTCTCGTAC CAACTCCTGA CGTTATTGAT	360
GCAGGGTCACG TAACGGGTT CCTGTATAACG GTACACTCTT CTTCAACTGG TCTAATAGTA	420
TTGCAGATCA AGAAAGATTT GCTGAAGCTT TGAAGCAAGA CGCAGATGGT AG	472

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

CTTTTAAATA AGAAGAACCA CACTCATTC TAAATGTGAT ATAATATTGT TCTCAGTCTC	60
ACCACTGGCT TGTAAAAAG CCATACTAAT CCCTGATTTT TCCGCATATT CCATCACCTC	120
AAGTGTGTTA CTCACTGAGC CAACTTGATT AGGCTTTATT ACAATACCAT CAGCACAATC	180
TTTAAACTGT GAAATTCTTT CTAAGTTGT TGCGTAAAAA TCATCACCAA AAACTTGTAA	240
CTTTAGAGGT TTTATCAATT GAAATTTCT CCAACTATCC AAATCTTCAT CGGAAAATGG	300
ATCTTCAAGA TAAACCAATG GATACTTAAC TCCCCAATCA CAATAAGTAT CCATAATTTC	360
TGTGACTGTC TGGTGCTGAC TAACACACCA TGGTACTTTA TATATGCCAA GTGAAGAAC	420
GTAACGATCT GTCATTGCTA AATCTAAACC GATATCATAT CTATTTTGAT ATAATTTAA	480
TGTCTCTAAT AACGAATCCA AAATAATATA AAAATCATCC GTGTTAATTAA TTAATGCACC	540
TTGATAGAAA TAGATGTTGT AGAAAACCTGG GTTTTAACCTT TATCATAACT CATTATATG	600
TTAGA	605

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

CTGAAGAAAA	TCAGTAAACA	AGAGCTGGTT	AACACCGCCT	TTTCTCGTTT	ATTTGCTCAT	60
TTTGGACAGG	AAAAAGACGG	TAGTTTCTT	GCCCAGCGTT	ACCAATTGTA	CCTCGCCCG	120
CAGGGACAAA	CACTATCGGG	CGCTCATGAT	CTCTTGACCA	GCCTCATTGA	GCGTGATTAT	180
AACTTGTATG	CTGCGACAAA	TGGCATTACT	GCCATTAGA	CAGGACGTTT	GGCTCAATCT	240
GGTCTAGCAC	CTTATTCAA	TCAGTCTTT	ATCTCAGAAC	AGTTGCAAAC	TCAAAAGCCG	300
GATGCTCTT	TTTATGAAAA	GATTGGCCAG	CAAATTGCTG	GATTTAGTAA	AGAAAAGACC	360
TGATGATTGG	AGATTCTCTA	ACCGCCGACA	TTCAAGGTGG	CAATAATGCG	GGGATTGACA	420
CTATCTGGTA	TAATCCTCAT	CACCTCGAAA	ATCACACACA	AGCCCAGCCG	ACTTACGAAG	480
TCTATTCTTA	CCAAGACTTG	CTGGATTGTT	TAGATAAAAA	TATTCTGAA	AGATCACGTT	540
TTAAGGAGAT	AG					552

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

CTTTGTCTGT	ATCTGCCTTT	TTATGCTATA	CTTAAGGTAT	GCATAGAAAA	ACAGTGATTG	60
ATTNTAGGAC	TTTAGGGGAG	AGATATACTT	TTACCCANCC	TATTAAGAG	TTGAAAACGA	120
GAAATGTAGC	AGAAGTGGCA	GATTTGCTGG	CACNAGTGGA	AAGCTACCAA	GAGCAAGATT	180
ATTATGTGGT	GGGGTATGTC	AGCTACGAGG	CTGCACCTGC	TTTGAGGAG	AAATTAGCAG	240
TTCACAAGGT	TCCTCTACTG	GCGAGTACT	TGCTTTACTT	TACTGTTCAC	GATAGGGTGG	300
AGACCTCCCC	TATTCCTCTG	ACTTATGAGG	ATATTGATT	GCCCTCAAAT	TGGCAGGGAA	360
NTAACGTCTG	CACAGAACTA	TGANAAGGCC	ATTGCCAGA	TACAC		405

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

CTCAAAAACA GCTTCTAACAA GCTTGAACAA GGGGGCTAAA ATTGATTCCCT TGATGTAGGG	60
TTTGAAGTAA GATAATAGGT GTTTCATAAA TCCCTTCTAT TCATATTCTA GAAATGAAGA	120
AAGTGGGAAG CCCCCACTCTC TGTTTTATTT GTTTAAGTAA GGCAATAGAT AGCCATATCC	180
TGCTTTTCTC ATCTCATCCT TGGCCACAAA GCGTAAAGAA GCAGAATTGA TACAGTAACG	240
GAGGCCGCCT AACTCCCCGCG GTCCCATCTGT GAAAACATGA CCCAAGTGAG CACTGCCTGA	300
ACGAGAACGA ACTTCATTG GCTCCATTCC ATGGCTCAGA TCCTTGTAAAT AATGAATCAA	360
CTCTTTGGAA ATCGGACGGC TTAAAACCTG GCCAACCCAC AACCTGAAGC AAACTTATCC	420
TTGGCAAAAA AGAGTTGGCT CACCTGTTCG TAATATCTAC ATAAATCCCC TCCTTCCAAA	480
GGTTTTGGTC CATAGGCATT GGTAATGGA CCTCCTGTTA CCAG	524

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

CTTCATCTGG TGGTTCTCCA GTTGTAAAGTA ACGTAGTACC ATTCTAAAA CCATACTCAC	60
AAGTTGGTAT TAAGGGGAA CCATATATCT TTAAAGGAAT GAAATGCAA AAAGATATTG	120
TTACAACAAA AGAATATAAC GAGGTTTAA AAAATGCCA AAAGAAAAAT TGGAATCCAA	180
TAGCAAATAC CAAAAGAAC TAGAAAAATA CATTAAATAA GGAATGGTAT TGATCTTGAT	240
AAAATTTTA AAATACTGTC ATTTTGAATA TAAAGGAGTT TGATATGGAG TGGATTAGAT	300
TAATAGGAAT AGCAATCATT GTTGTGGTT TTATTTAAA ATTTGATACA ATTGCAACAG	360
TAGTCTTAGC TGGTTGGTT ACAGCTTGTGTTTCAGGTGT TTCTCTCGTT GAATTTTG	420
AGATTTGGG AAAAGAATT AGCAATCAGC GAGTGCTCAC GATTTTATG GTTACCTTGC	480
CTCTTGTGGG GCTGTCAGAA ACCTTGGAC TCAACAAACGA TCAATCGATT TGATTCGAAA	540
GATTAAAGGT CTGACAGTTG GAAACTTCTA TACAGTTAT TCTTTATCGA GAG	593

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

CCTGCTCCCTT ATCTTTGCAG TAATTGGCGT TTTAGTGGCC TTGATAGCTC AATTTTACTC	60
AGCAAAGGCA GCAGTAGGTT TTGCTAAGGA ATTGACAAAAC GATCTTTATC GTCATATTCT	120
TTCCTTGCCC AAGGACAGCA GAGACCGTCT GACAACCTCT AGTTTGGTTA CTCGCTTGAC	180
TTCGGATAACC TACCAAGATTC AGACTGGTAT CAATCAATTC CTGCGTCTCT TTTTACGAGC	240
GCCCCATTATC GTTTTTGGTG CCATTTTTAT GGCTTATCGA ATCTCAGCTG AGTTGACTTT	300
CTGGTTCTTA GTCATGGTTG CCATTTTGAC CATTGTCATT GTTAGGGTTA TCTCGATTGG	360
TCAATCCTCT CTACAGTAGT CTCAGAAAGA AAACCGAACC ACTGGGTTCA NGAAACCCCC	420
CNCCATTGCA AGGATGCCGG GTTATTCCGT GCCTTT	456

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

CTTGTACAGT TGAATCGTTC AGATATTGAT TTTGAAAACA GAGAGTGTGT TGTCTTTGGT	60
AAAGGAAAAGA AGGAGAGACC AGTATATTTT GACGCTCGGA CGAAAATTCA TTTAAGAAAAT	120
TATCTTAACG ACAGAAAAAG ATAGTCACCC TGCTCTTTT GTAACGCTAG TTGGAAAAGC	180
CCAGAGACTT GGAATTGCTG GTGTAGAGAT TCGCTTAAGA AAGTTAGGAG ACAAACTCGG	240
CATACAAAAG GTTCACCCAC ATAAGTTCAAG AAGAACTTTA GCGACTAAGG CAATTGATAA	300
AGGTATGCCT ATCGAACAAAG TCCAAAAACT GCTAGGTCA AGCAAGATTG ACACAACCCCT	360
GGCCTATGCC ATGGTCAATC AAAATAATGT CAAGCATTCAC CACCAAAAT TCATCTCTTA	420
AAAGCAAATC CCGATATTCC GAAGAGGTGG TTGCATGAAG AAAGTGAAT TAGGTGAAGT	480
GGCTACTTTT ATCAATGGCT ATGCTTTAA ACCTCAAGAT TGGTCCTCTG AAGGAAAGAG	540
ATTATCCGAA TTACCGAACATC TGACT	565

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

CTTTATACTT TATCATTCT AACTTAATTA TAGTCTTATT TTTAATAAAG TTCAATTATT	60
TATATGAAA ATTCCTCATC AGTAAAAAAT AACCGATCTC ATTTCTGAGA ATCGGTTTC	120
TAAATAAAC AAACCGATCA TTTACATAAC ATAAATTATG TAAATGATCA TACTACAACA	180
ACAAATCTT GACTTTCCA ATTTCACTTT TTGGAATAAC CAGGTGAATC ATATCACCCA	240
GATACATTCT GGTTGAGCCG TTAACGTGTT GGCTCTGCC ATTATGGACT TGAGTTGTGA	300
TGAGGACGTT GTGTGGTAAG TTGAGTTCAT GAACTTGTTT CCCAGCAATT TTATCAGAAA	360
CTGGTATTTC GATAAGTGTAA CTCTCTCCTT CGCTAGATAC TTCTTCTGGG AAGCATTTTT	420
TCCAGCATGG CTTCATAGAC TGGCGTTCCCT TTGAGCNAAT CCCTGATNAT TTTAGAAACC	480
AGAGTGACAG ACCAGTGGCT TAAGGTGCGA ATATCTCCTA CCATCTCAGT TACGAGAT	538

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

CGTGCTAACC ATGAGAGCAT ATATTCCTC CAACTATTTC TATTTCAAAA AATCCTTACT	60
ATATTGTATC ACAATCAGAC ACAAAAAGAA AAAGCAAATG ATAAACAAAT GCTTTTAANG	120
TTTTAAAAAA AGCTTCGAAA GGTTCTTCTT TATTTTTTAA NGGGAGAGAT AACGTTGATA	180
TCTAAATCGT GGTCAAAGCC GGCAATTTC CTTTAGATGT GTATTGGTGA ATATCATAAT	240
CTAAATCAGT TTTAGGACTG CTCTCCAAAA ATCCTGAGTC TGAGCCGTAG GACGGAATCC	300
AAACAGAGGT AAACTTGCCT GTATCAATAC TGTGTTCTTC CATGAAGTAG ACACCAACGT	360
AGATGCCGAT GTTTTTAGCA CCTAGTGATG CTAGTTTGC TCGAAAGTTT TCGACACCTT	420
CGTTCATATA GACATAGTTT TGTCTCCACG TCAGCCCATA GTAACTAGGC TGTTAGGAGA	480
GCACATTGTA GAAAATTCG GCAGCCTTT	509

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

CTGTTCTGTT	TGCGACGCTA	CTTGGTTGTA	GCATGGGGGT	GGTTTTAGAT	GGTCAGTAAG	60
TATCTTTTAT	TAGCAGTTAT	TTTCTCTGGC	TTGGTGAATT	GGATTCTCCG	TATGATTTCC	120
TTCATCTTAG	TCAAGTATAA	GGGCTTGCCCT	GCAATCGTTG	AGCGTTTTTT	GAAGTTCTTG	180
CCCGTTTCCA	TTATCTTGC	CTTGATTCTT	TCAAGCGTAG	TGACAGGTAA	GGTTGGGAGC	240
CTTCCTCAA	TTAAATGGCT	AGACTTCTTA	GCCGTCTTTC	CAACAGCTTG	GGTAGCCTTT	300
CGCTACCGCA	ATCTACTCGG	AACAGTTCTC	TTTGGAGTGG	TCTTGATTGC	CATCTTGCCT	360
TTGGTCTCTT	AAATTACCCA	CCAAAAAAAAC	TTATCACAGA	GATAGATATC	ATATAATGGC	420
GTAAATGCTC	CTTTCTGTT	AAAGATTATAA	GGTATTCTAT	TTTGGAGGAA	ATGACATGAA	480
AAAAATCGTT	AAATACTCAT	CTCTTGCTGC	CCTAGGACTT	GTTGCTGCAG	TGTGCTTGCG	540
GCTTGCTCAG	GGGTGCTCAG	AAAGAAGAGA	AC			572

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

CTAGGTTATT	TAGTAAAAGA	CTAGAAAGATT	TTCTTTCCC	AATCGTCTTC	TGTACGGCGA	60
GGATAGAAAA	ACTCTGACTT	GTCGGGAGCT	TCCATCATTT	CCATCAATGG	TAGCATATCA	120
TAGGCCAGAT	TTAAGTTGG	AATCTGGTCT	TTTGACCCC	AAGAAACTTC	TCCCTCTTCT	180
GAAGATTGAA	GGGTACCAGA	GAACTCAGTC	GCCTTATAAC	AAATGACAAT	ATAGCGCCCA	240
CCTGTATCTA	GTGGCCAATT	TTAATGCCG	ACAAGTTGAG	GATTTGGAT	AGTCAACCCCT	300
GTTCCTTCGT	AGATTCACG	AATGACAGAC	TCCGAAAG	CCTCATCATT	TTCTACATGA	360
CCTCCAGGAA	AGGCATAACC	AGACCACCGA	TIGTTTCAG	GGGCCGATA	CTGCATCACC	420
ACGCGCTGAG	TTTCGANGTC	TTCCATCAGA	CAGATATTG	TTTAAATTGT	TTAATTGGGA	480
ACGGGACATA	AATTTCAC					497

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

CTGAAATTTT GGAAGAAGAA ATCGGTGTAG ATACAGTCCA AAAAATAGGA CGCATCTTGA	60
TTTTGTTTAA ACAATCTAGC AAGAAAGAAA ATCGCAAGAT TTCTAAGAAA GTCAAAGAAA	120
TCTAAGATCG AAACCTCCAAA TAACTGTTT TATAGAGAAA TAAAGGGGAC TAGCCTATGA	180
CAATCGAACT ATTGACTCCC TTTACCAAGG TAGAGTTGGA GCCAGAAATC AAGGAGAAAA	240
AACGAAACA AGTTGGGATT TTAGGGGGGA ATTTTAACCC TGTCACAAT GCCCATCTCA	300
TTGTTGCGGA TCAAGTACGG CAACAGTTGG GACTGGATCA AGTTCTGCTC ATGCCTGAAT	360
ACCAACCTCC TCACGTTGA TAAAAAGGAA ACCATCCCTG AACACCATCG TCTCAAGATG	420
CTTGA	425

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 418 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

CTGCTATCAA GACAGTATTAA CCGCTGAAAG AAACAGCTTC ACTAGAAGGC GCAATTGAAA	60
ATAAAGACGG GATCACGAAC TCCCCTTTT CTATAAAAGA AAGGAAATGG GATGAAAAAA	120
TTAGTCTTTG TCTGTCTGGG AAATATTGCG CGTAGCCCTA TGGCCGAGTT TGTTATGAAA	180
TCAATGACAG ATAACATACGA AATCCAAAGT CGAGCAACTT CCTCTGGGA ACATGGCAAT	240
CCGATTCTATA AGGGGACTCA GGGAAATTTTT CAAGAGTATG AGATTCTTA TGACAAGAAC	300
AAGACATCGC TTCAGATTAG TAAGGAAGAT TTTGAAGCCT TTGATTATAT TATCGGAATG	360
GACGCTTCAA ATGTTCCGAC TTACGTCAGA TGTGTCCAGT AGACTGTCAA GATAAGAT	418

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

ACTGTTTGAA	AAATATGATT	CGTGGTCGAG	AAATGAATTG	CATTAAAGCA	ATGTAGTTCA	60
GTATATAGAT	TTGGAAATTA	ATGATTTAAC	AAAATAAAGG	AGAAAAAACCA	TGGTTAAATA	120
CGGTGTTGTT	GGAGCAGGGT	ATTTGGAGC	TGAATTGGCT	CGCTATATGC	AAAAGAATGA	180
TGGAGCAGAN	ATTACTCTTC	TCTATGATCC	AGATAATGCA	GAGGCAGATTG	CAGAAGAATT	240
GGGAGCAAAA	GTTAGCAAGT	TCCTTAGATG	AGTTGGTTTC	TAGCGATGAA	GTTAGATTGT	300
GTTATCGTCG	CAACTCCCAA	ATAATCTTCA	TAAGGAACCG	GTTATTAAGG	CTGCACAGCA	360
TGGTAAAAAT	GTTTCCTGT	TGAAAAAA				387

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CTTATGAAAT	CAATCATCAA	AATAATATTG	ATCAGGACTA	TTTAGGTAAA	TTATCTACAA	60
CGATTAATT	GGTAGCAGAA	AAGGAAAATG	CCGTTGAGAT	CCTAGAACAC	TTGAATGTTG	120
TCCCTGTGTT	GACAGCCCCAT	CCAACACAAG	TGCAACGCAA	AACTATGTTG	GATTAAACAA	180
ATCATATTCA	TAGTCTTTG	CGTAAATACC	GTGATGTTAA	GTTGGGGTTA	ATCAATAAAG	240
ATAAAATGGCA	CAATGATTTG	CGTCGTTACA	TCGAAATTAT	CATGCAGACCA	GACATGATTG	300
GTGAGAAAAA	ATTAAGTG	ACTAACGAAA	TCACGAATGC	TATGAAATA	TTACAACAGC	360
TCCCTTTTGA	AAGCTGTCCC	TCATTTGACG	ACGGAGTATA	AGCGCTTAGC	GCAAGCGCAT	420
GGTCTGAATT	AAAAACAGGC	AAACCAATC	ACCATGGGTA	TGTGGATAGG	TGGTGACCGT	480
GAAGGAAATC	CATTTGTTAC	AGCAAAGAAC	TTGAAGCAGT	CTGCACTCAC	TCAGTGTGAA	540
GTCNTCCTGA	ACTTACTATG	A				561

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

CGACCTAATC ATATTGATAC TGCATTTGCA TCAGCGAGATT TGTTTGAGTA TAAATTACAA	60
TTACCCAGGAC AGACTTGGGG ATATTTAGAA TTGAAACAA ATACAGAAAA ATATGGAAA	120
GTATTGTTAA TTATAAAGGG TAAGAACGCA CTTACGAACC AATTTCCCTTT GGTACAAAAAA	180
AATAAAGAGTG GCTACTTATT TGAATATGCT CAGATGAATA CACTTTATCT TAATCAACAT	240
TCTTCCTACA AAAATGATGA AGATAGTCAT TCCTTCCAA TTCAGATGGA GTTAGTTCT	300
GATGAAATGA TTCCAAGAAA TTGAACAAGC TACTAAAAAT TCCGAATATC CGAAAAATTT	360
ATGATTTTAA CTTATGANGC GGACTCCCGA AAAACAATAT TATATCTGTT AGATGTTGT	420
TATGCCCTGA TGCCCGAACT GGTCCAGTTA CACTTGATTG CAGATTGTCC TGAGTATATC	480
CATCCAGTTG CGTACC	496

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

CCACCCCTCTA GCAAGTGGTG CTAATTCCTA TAGCCTAGAA GAAAACGAAA TCATCTACCA	60
AAAGTTAAAA AACTTGCTTA AAAACTGATA AAATACTTGC CAAACTTTTC AGAATCTGAT	120
AGACTAGTAT GGTAACAATC TATGGCTCGC AAAGAGACCA TGGCAGAAAG GAAATATTGC	180
AAAATGAAAA AAGATATCCA TCCAGAATAT CGCCCAGTTG TCTTCATGGA CACAACACT	240
GGTTACCAAT TCCTTAGCGG TTCAACAAAA CGCTCTAACG AAACAGTTGA GTTCGAAGGC	300
GAAACTTACC CATTGATCCG TGTGGAAATT TCATCAGACT CACACCCATT CTACACTGGA	360
CGTCAAAAGT TCACTCAAGC AGATGGACGC GTGGATCGTT TCAACAAAAA ATACGGTCTC	420
AAATAATGAT AAGAGAACAG TTTCGGCTGT TCTTTTTTGT TTCTTGAAAT CAACTGCTGT	480
TTTCATGTTC CAGACTCATC TGTA	504

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

CTCAGGCGAT TACTAATTAC ATGACTTCTG CCTCAAAC TT TAATGTCGAT GAGGCTAGCC	60
AATTCAATTCA ACAATTTACA ATTACAAAAC AAATCGAAC AGTAGAAAAA CTATTAGAGG	120
AGTAGCATGG AAACTGCATT AATTAGTGTG ATTGTGCCAG TCTATAATGT GGCGCAGTAC	180
CTAGAAAAAT CGATAGCTTC CATTAGAACAG CAGACCTATC AAAATCTGGA AATTATTCTT	240
GTGATGATG TGCAACAGA TGAAAGTGGT CGCTTGTTG ATTCAATCGC TGAACAAGAT	300
GACAGGGTGT CAGTGCTTC TAAAAAGAAC GAAGGATTGT CGCAAGCACG AAATGATGGG	360
ATGAAGCCAG GCTCACGGGG ATTATCTGAT TTTTATTGAC TCAGATGATT ATATCCATCC	420
AGAAATGATT CAGAGCTTAT ATGAGCAATT AGTTCAAGAA GATGCCGATG	470

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CTTATACTTG CTTTTTTCCCT TTTGAAAAT GTTAATAAAT CGTTGGTAGT CTTCTCTAGG	60
CATGGACAGA TCAATATCGT CGTCCAAGG GATAAAGCCC TCATGTCGAA CCGCCCCAAT	120
CAGAGTACCG TAGTTAATAA TATAGTTGAT ATTGTGCTTT TTACAGAGAG TATCAATATA	180
ATCCAAAATT TCTAATTCAA TTTGTTGGC ATCTTCATG GTTAGTTGTT TCATTTAAA	240
CTCCTATGAT TTTTGAAATT TATTTTTAA GGCTAGGACA TGGTTAAAA ATTCAATAGAA	300
AATGCTATCT TTTGTGAAGA CAAGTAGACT AATATAAGAG ATAGCTGATA ACAAGACAAT	360
CAAACCAAGTA TTAATCAAAA ATGGCAAATT AATGACCATA TCCACAGGAT ACACGAAATT	420
AATCAGGAAA TACATTGCTA CAAAGGAAAG TGAAAAGAGA GAGTATCGAA CAGTATAGCT	480
AAAGATATGT CCCAAGTGGG TGAGTTGTTT CTATGGATGA AATGAT	526

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

ACCATATCAA TACTATCGAA AAGTACAAGG GATNCAGTCT CAAGGTCGCT GAGGAAGATT	60
TGAATGACCT AGACGATGGT GAATTTACT ATCACGAGAT TATCGGTTG GAAGTCTATG	120
AGGGTGATAG CTTGGTTGGA ACCATCAAGG AAAATCCTGC AACCAAGGTGC TAATGATGTC	180
TGGGTGGTCA AACGAAAAGG CAAACGTGAT TTGCTTTAC CTTATATCCC ACCAGTGGTT	240
CTCAATGTTG ATATTCCAAA TAAACGGTC GATGTGGAAA TCTTAGAAGG GTTAGACGAT	300
GAAGATTGAT ATTTTAACCC TCTTCCAGA GATGTTTCT CCACATGGAGC ACTCAATCGT	360
TGGAAAGGCT CGAGAAAAAG GGCTCTTGG ATATCCCAGT TNTCATAATT TTTCGAANAA	420
AATGCTGAAA AGG	433

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

CTGCAACTTG AATTTCTCCT TCTTGTTCA AAGCAAGATA AACAAATTGCA GCCCCTCTTT	60
TTTCTAGCAA ATCCCCCATC TGGACAGATT GCATAAAGGA ACGAGAAAGAA ACCTGATCAG	120
AATAAGTCTG AAACCTCTTCT TTCGTGAGTG TTGTTAGTGC CATATACTTA CTTTCTATGT	180
TTTTTTCTTA ATGTTTACG GAAATCAAGA GCAAGTCTTA ACAGAGGATA GAGAGGATGA	240
GTGGGCATTG TAAATTCAACC CAAGTATTCT TCAATCGTTG GATTAAATTG TTCTTAAAAA	300
TGATAAAAGTC CACCATTGAG AGAGTTTCA ACACCACCTA AATTTGCCA GACCACACCT	360
CGCTCAAAGG CATAGCGAGC CGTTTCATAC CATGTTAAAAA TTGGTGCATT GTAACGTTA	420
AAATCATCAT CCATACCCAGC ATATATATTG ACAGAGGTAG TACCAAATTC CAAACTCAAA	480
GTACCGCTAA AGGAATCTCG CTTGACCTAC ATCTATATAT TCCTGCAAGA AGGTCAATT	540

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

CTCAGGCTAA AAGAGTCCAC TGGACTCTTT TACTCCGTCC CATAACCAAT GACTTAATGG	60
CGCGTTCAGC TAGATTATTG GAAAGGACCA GATGTCCGTC TTTCAAAATA GTCTTAAAGG	120
TTTCTTCATA CTTGAGGCTG TATTCAATTG CCCTTCCTAG TTTTGAACCC GATAAAACTG	180
ACTGACGCCG GCACCAAGCA AAGAAATCTT CCATTAGGGG TTGGAGCTCT TCTTGACGTT	240
TCTGTAGTCG TTCATCAGCT GACAATGTCT CCCAGTCTCT TTCCAAGGCA AATAACTGAT	300
CACAATAGGC TAATCCTTTA G	321

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

CTTGACCAAA CAAGGCAGTT GGAAATTGAT TTTGGAGGAT GAGAGCGCTG GAAGGGAAC	60
CTTCCAATC TTGACTCAAG GTCNATATAT CGCAACATTT GACCAACAAG CGCCANCTAT	120
CGATGAAATC TTTAAACTAT AACCAAGGAGT GGAAGTATGA GAAATATGTG GGTTGTAATC	180
AAGGAAACCT ATCTTCNACA TGTCGAGTC TGGAGTTCT TCTTTATGGT GATTTCGCCG	240
TTCCCTTTT TAGGAATCTC TGTAGGAATT GGGCATCTCC AAGGTTCTTC TATGACTAAA	300
AATAATAAAG TGGCANTACT GACAACAGTG CCATCTGTAN CATAAGGACT GAAGAATGTA	360
AATGGTGTAA ACTTCGACTA TAAAGATGAA GCAAGTGCCA CCAGAAGCAA TTAAA	415

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

CTATNAAATA GAGTGGTTCT CTATCTGCCA TGACCACAAA TNAGGACAAT GATACTCTG	60
AACGTTCAGA CTGCTATCGT AAAAGGACAG CGGGTGAGAC GCCCATGAAT GATCTAACCA	120
GTCATACCCA CGGAGGAAAT TATACAATAG CACGTTATCA GGAGGAAAAA TTTTGGAAACA	180
AACAGTTGTA AAATATAGTC TGCAGTTATC AATGCTTAAT TTTTACAGG CGAAGATAAT	240

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

CTTGTCA	TCC	TCACGAA	AAT	TGCGATTG	T	AAGCACCA	AG	CCTTGACT	CG	TGATAGACT	G	60		
AATCATG	C	CTCTCATG	T	CTCCTCA	AGT	CGTTCATG	G	CTTCTTG	GAT	AGTCTCC	CAT	120		
CTGGCTG	CAT	AAGATAGG	CG	GACGTAGC	C	TCCCCGTA	AC	GTC	CAAAGG	TG	CACCAGG	G	180	
ATAAAGC	AA	CCGCCTT	C	CTGAGC	AAA	AA	TCCTTCAG	AA	AAGCAAAGG	G	TGCTTGATT	G	240	
TAGCCC	GCT	G	GAATTTT	AGC	AAA	AA	AAGGCACCG	GT	CTGGTTG	A	ATCTCA	AA	300	
CCAAGAGC	CAG	TCATTTT	MIC	GATGAT	ATAG	TCCC	GACG	TT	GGATATATT	C	TTCTTCAT	G	360	
GGCTCC	G	C	CGTTTTT	A	AGCCG	TCA	AG	GCTT	CTACCG	CAGC	ATGTTG	CGCC	420	
TTTGGG	CAG	TGACCA	AGTT	ACTGGT	GACT	CTT	GATTA	AC	TGGG	CTGT	G	AGGT	NCANG	480
AGCAAA	ATC	AGCCC	AAAC	GCC	AA	CTGT	CAT	GG	GG	GTG	TA	AG	TC	519

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

CTTCAGCT	TAT	TCGTGGG	A	TAT	TTAGATG	TAC	TT	ATTT	TAGG	G	TGAA	ATCA	TAT	GAATATT	60			
ACCA	AT	TTG	TGT	TT	TCT	TAT	CAA	GAC	AGG	GAT	G	TAT	GGCA	ACT	GCAAA	AACTA	120	
TTTT	TCAG	T	TG	GGAT	TT	TACA	AT	GGG	GAG	AA	TG	AC	AG	ATC	AA	TTAGATT	C	180
AATT	TTG	TTC	CTCG	TAG	TCA	AT	TTG	TAG	AC	GTG	G	ATG	ATG	T	GA	ATATAAA	AA	240
GAA	TTT	AA	CT	AT	TTT	TAT	CTT	CC	AC	TG	A	ATG	ATG	T	AG	AAAGTTT	GGT	300
TT	AT	ATG	ATT	GG	TT	CC	AC	AT	GG	AT	TT	AA	AG	TTT	CC	GAT	CCGT	360
AT	GG	CT	CC	AT	TT	CC	AC	AT	GG	AT	TT	AA	AG	TTT	CC	GAT	CCGT	420
AA	AC	AG	CC	AT	AC	CC	AC	AT	GG	AT	TT	AA	AG	TTT	CC	GAT	CCGT	468

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

CTTGAATAGT CTCATCACGA AAATTGCCAT AACTGATAAA ACCAACCCACC TTCA	60
CACCGCCAT CAATGTATTT TCTGGATACT TTTCGACTAAA GAATCGACAT CTTTCTAATG	120
TCATTGTATC CTGAAATTCC GCAGGCAGAA GGTCATCATA AGACTCTCTC CACGTTGCC	180
AGTGAACGAG GGATTTGCCCT TCTATCTCTT CAGGAGTTNC CATAGATTTG ATAATAACCG	240
TCATTTATTT TCTCCCAGTC TNCTCTCAAAT ATACCATATT TAATACTATC AAAATATTAA	300
CCTTGATAAT AACGAACTTT NGGAATATGA GCTNCTTTTC TCATNCTTAA TTTTCAGCA	360
AGTTTCATCA TACCAAGATT TCCTGACCAA GTTGTCAAAA CCAGATGCTC CAACTCCAAG	420
TAATCCTGAA ACGTCCTATC TATCCACTGC AACATAGCAA CTTTCCCAAT ACCAGTGTTC	480
CAGAATTTTT TATCATAAAAT ACCAATTCCC AATCCATCCA TCTTGTTC CTTACATACC	540
CAATA	545

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

CTTGATTGTG GAAGAAGTCC GTGATCGCTA TGTGGGCAAA GTCGATGCCG TTTTCATAA	60
CGCGGATTCT GAACATACGTC CGGATTCTCC ACTTGGGAG GGCATCCCG TTGTTAAAGG	120
GAACATGGAC TTCTACGCCG GCTACCCAGA ACCTCTGGTG ACTGAGCTTG GTTCGACCAA	180
GATTATCCAA ACTCATGGTC ACTTGGTGA CATCAATTTC AACTTTCAAAGTTGGACTA	240
CTGGGCTCAG GAGGAAGAGG CCGCTATCTG CCTCTATGGT CACTTGCATG TGCCAAGTGC	300
TTGGTTGGAA GGCAAGATCC TCTTTCTAAA TCCAGGCTCT ATCAGTCAAC CACGAGGTAC	360
CATCAGAGAA TGTCTCTATG CTCGTGTGGA GATTGATGAT AGTTACTTCA AAGTGGACTT	420
TITGACACGA GATCACGAAG TGTATCCAGG TTGTCCAAGG AGTTAGCCG ATGATGCCAA	480

GGAGTTGAGA CTTTCTGTTG GGGCAGAGAA CTTTTGA

517

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

CGTAACCATT	AACTATGAGG	TGGTTTGCCT	CCTCAGCGAC	CGTATTCCGA	GAGAATATTA	60
TTAGAAAAGA	AAGGAGTGGA	GCATGAATCT	ACATCAACCC	TTGCATGTCT	TGCCTGGTGT	120
GGGACCAAAG	TCAGCAGAAA	AATACGCCAA	ACTAGGAATT	GAAAACITGC	AAGATCTCTT	180
GCTCTACTTT	CCTTTCCGTT	ATGAAGACTT	CAAACCAAG	CAGGTGCTGG	AACTAGAAGA	240
CGGTGAGAAG	GCAGTTCTTT	CTGGTCAGGT	AGTGACTCCT	GCTAGTGTCC	AGTATTATGG	300
TTTCCAAGCC	GCCAATCCGC	CTGCGTTTTT	AGTCCTCCAA	GCCAGGGAAAG	AAGGTTCGTT	360
TTTTTTGGC	GGGTGAAATT	TCCTTTTAA	CCCAGCCCCC	TATCCTTGGG	CTTGAATAAA	420
AAATTAGAAA	TTTTGGGAA	CCAACCCCTT	TGGCTTGT			458

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

CCTTACTAGT	TTACTCAATC	TTTACATCGT	TCTTCGGCA	GTTCAAACTC	AGAATCCACA	60
GCACAGGTTA	TGCAATTACT	GTCTGAAAAT	ATGTTAAAAAA	CCATTCAGTC	ACTTTCGGTC	120
TGGCAGATTT	ATTTGCTTGG	TTTGAGCGA	ATCTTGGCGC	TTGGTTTCCA	ATTACTTTG	180
ACAGTTTGGG	TTTACCAAGC	TGTTCCCGAG	AAGAAATGGA	TTTATCTCCT	AGCAGCCTAT	240
GGCTTGCATG	CCTTCTTTGA	TCTGGCACCA	TCTCTTTCC	AAGTAGGCTG	GTTGACAAAT	300
CCAGTCTTGG	TTGAAGTGAT	TCTAGCACTG	CAGCTCGTTC	TGGTCGCCCTA	TGGAACCAAG	360
GAAATCTTTT	GTAAAAAATC	ATAAAAAGGG	GGGAACCTCT	TTTTCTTATG	CAAATCCAA	420
ACAAGGTATT	TTTATGGTCG	TCAAATGTCT	C'AAAAAATGG	TATAATGGAA	TGAATTTGT	480
AAAAGGAAGA	ATGACATGTC	TGTAAGAGAA	AAAATGTTG	AAATCTTAGA	AGGAATTGAT	540

ATCCGTTTA AGGAACCCTT GCATAG

566

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CTTTGACAAA GAGTATGACA CCTGACCGTG AAGTCATTAC CTTTATTCCCT GAAAAATTAA	60
TTGTGGATGG TTTCCAAGGG ATTCTGTGACC CACGTGGCAT GATGGGGTT CGCCTTGAAA	120
TGGTGGTTT GCTTTATACA GGACCTCGTA CTATCTTGCA CAATTGCGT AAGACGGTTG	180
ACCGTGCAGG TGPTCAGGTT GAAAATGTTA TCATTTCACCC ACTAGCAATG GTTCAGTCTG	240
TTTTGAACGA AGGGGAACGT GAATTGGTG CTACAGTGAT TGATATGGGG GCAGGTCAAA	300
CGACTGTCCG TACAATCCGT AATCAAGAAC TCCAGTTCAC ACATATTCTC CAAGAAGTGG	360
AGATTATGTA ACTAAAGATA TCTCCAAGGT TTGAAAACC TCTCGCAAAT TAGCGGAAGG	420
CTTGAAACTG AATTACGGGG AACCTATCCG CCTCTTGCAA GCAAAAAACT CCATTAAGT	480
TATTGGAGAA TTAAACCACT CAAAGTGACG GAACTACTT GTC	523

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

CTGTGATTTTC AGAGAAGAAA TCAAGTGCTG TAACAGAACT AAGATGTAAT TGTATGTA	60
GGAGACGTCA TGTAAATAG TATTGTAACC ATTATTTGTA TTGCCCTTAT CGCGTTTATC	120
TTGTTTTGGT TTTTCAAAAAA GCCTGAAAAA TCTGGACAAA AAGCCCAGCA AAAAAACGGA	180
TACCAAGAGA TTGAGTGGG AGTCATCGGA GGCTATACTC CTGAGTTGAT TGTCTCAAG	240
AAATCAGTGC CAGCCCCAT TGTCTTGAC CGCAAGGATC CTTCACCATG TCTGGATCAA	300
ATTGTTTTTC CAGATTTGG TGTACATGCG AACCTGCCAA TGGGGGAAGA GTATGTAGTG	360
GAAATCACGC CTGAACAGGC TGGAGAGTTT GGCTTGCTT GTGGTATGAA CATGATGCAC	420
GGCAAGATGA TTGTAGAGTA GGTGGAGACT ATGACAGAAA TTGTGAAAGC AAGCTTAGAA	480

AATGGCATTC AAAAAATCCG TATCCGAGCT GAAAAAGGCT ATCATCCACC CATATCCA 538

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

CCTCAAGAAG	TCCGCGATAC	TTACGAAAAT	ATTTTGTAGA	GAATCGAACCC	GCAAGGTTCG	60
GTTTTCTTTC	TCTTTTTGTC	TATAATTGG	TATAATAAAC	AGTATGAAA	TGTTATCAGG	120
AATCTATGGG	GGACGTCCCC	TCAAGACACT	AGAAGGCAAG	ACAACAAGAC	CTACTTCGGA	180
TAAGGGTAGG	GGAGCCATT	TTAACATGAT	TGGTCCCTAC	TTTGAAGTGG	GACNAGTCTT	240
GGACCTTTAT	GCAGGTAGTG	GTGGTTTATC	TATCGAAGCA	GTATCGCGTG	GCATGTCCAG	300
TGCTGTTTTG	GTGGAGGGAG	ACCGTAAGGC	TCAGACCATC	GTGGCTGAAA	ATATCCAGAT	360
GACCAAGGAA	GTGGAAAAT	TTCAACTCCT	CCAAAATGGA	TGCAGAAAGG	GCATTGGAAC	420
AGGTTNTCTG	GGGAATTGAA	CCTCGTTTTC	TTAGACCCCTC	CCTATGCCAA	GGAACAAATC	480
GTAGCAGATA	TTGAAAAAAAT	GGCTGAGAGA	GAGCT			515

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

CTGGANACAA	ACTTTACAGA	TCAAGTCGAT	ACGATGATTT	ATGTTGATAA	AGAAGAAGAA	60
GAAAATTTA	AAGCTGCACT	TGTGGAGTTT	TTTAATGGAA	AAGTCACTTT	AACTGACCAA	120
GGTTTACGAG	AGGTTGAAGT	TCCTGTAAAC	TTAGTGTAAA	CAATGAATAA	TACAGCGTTT	180
CGTTGACATT	CTCACAACTA	CTTTAGCGAG	CAAAATAAAA	AGATGCGTAC	CAAAATATAC	240
TAGAAAATGA	AGCAATTCAA	ACGAAACCTG	ATATCGTTTT	CCTTCACACC	TATTTACTAG	300
AATTAACGTGA	ACGCAATCAC	TTGAAAATTA	ATGACTTTGG	AT		342

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

CTATTAGCGA	CTTTCTCTGA	AATATGGTAT	GATAAAGGAT	ATACAAGGAG	ATAAAATGAA	60
TAATAATTAA	CTGGTATTAC	AATCCAGACT	TTGGTCTGGT	TGATGGTGGC	GTATCGGCTA	120
TGATTGGAGT	GGCTTTAGAA	GAGTCCTCAA	CCTTAAAAAT	CCATCACTTG	ACGCACGATA	180
TCACGCCCTA	TAATATTTTT	GAGGGGAGCT	ATCGTCTCTT	TCAGACCGTG	GATTACTGGC	240
CTGAGGGAAC	GACGTTTGTA	TCGGTTGTCG	ATCCAGGTGT	CGGTTCGAAA	CGTAAGAGTG	300
TAGTTGCCAA	GACTGCTCAA	AAAATCAATAC	ATTGTCACGC	CAGATAATGG	GACGCTTCC	360
TTTATCAAGA	AACACGTTGG	CNTTGTANCC	ATTCGTGAGA	TTTCTGAGGT	GGCCAAC	418

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CTCTCGCTTT	TCTCATAGTG	GGAGGTAAGG	ATGGAATTAC	GCAGACCAAG	ATTAGCGGAT	60
AAGAAAGCTG	TTTTAGATAT	GATGACAGAG	TTTGAAAAGA	GCCAATCAGC	CCATGATGGA	120
GGAATTGGGG	ATACAGAGAA	TTTTGTGTAT	GAAGAGTGGT	TGGAAAGCAA	TCAGGAACAG	180
GAAATGGGGA	TTAATCTGCC	TGAAGGATGG	TTCCCTGCAA	TTCAGTTAGT	GGCTTTTCT	240
GAGAAAGGTC	AAGCAGT'GG	ATTTCTTAAT	CTCCGGTTGC	GCCTCAGTAA	CTTCTACTA	300
GAAGAAGGTG	GGCACATTGG	CTACTCCATC	CGTCCCATCTG	AAAGAGGCAA	GGGTTATGCA	360
AAAGAACTCT	CCGTCAGGGC	TTGCAAGTTG	CTAAGGAAAA	GAACATCAAG	AAAGCTCTGG	420
TGACCTGTAG	CGTGAATAAT	CCTGCTAGCA	GAGCATCATT	CTA		463

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

CTCTTACGTG ACCAGAACAT GCTACTTCCC ATCCGAGAAG CCATTCTATC TGGCTTACCA	60
GTGTTGGGA CCTGTGCGGG CTTAATTTCG CTGGCTAAGG AAATCACTTC TCACAAAGAG	120
AGTTATCTAG GAACTATGGA TATGGTGGTC GAGCGTAATG CTTATGGCG CCAATTANGA	180
AGTTCTNCAC GGAAGCNNAA TGTAAGGGAG TTGGCNAGAT TCCNATGACC TTTATCCGTG	240
GTCCGATTAT CAGTACTGTT GGTGAGGGTG TANAAAATTCT AGCAACAGTG AACNATCAAT	300
TTGTTGCNNC CCAAGANNAA AATATGTTGG TAAGTCCTTT TCATCCAGAA TTGACTGATN	360
ATNTGCGCTT GCNCCAGTAC TTTATCAGTA TGTGTAAGA AAAAAGTNGA GATTGAATTT	420
CTCCAACCTT NCCACNTGTA ATNNNCAATN NCNATGTATT GGAGTACGGA CGCAG	475

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

CCTTCAAAAA TTATTTGATG CAACCTTAGA CAATCCAGAA CTCACCGCAA CATTAGTGCC	60
TTTAGGAGAT GGTATTCTCA TGCTTCGTA AAATGTAGCA GATGTTCAAC TGTCTGAAAG	120
CGAATGATTT TCAGAAAAAT TTAAGAAAAA ATAGTAAAT AGATAGAGTA ACACATTATCT	180
CAAAGGAGTA GACATGAAGA AAAAATTATT GGCAAGGTGCC ATCACACTAT TATCAGTAGC	240
AACTTTAGCA GCTTGTTCGA AAGGGTCAGA AGGAGCAGAC CTTATCAGCA TGAAAGGGGA	300
TGTCATCACA GAACATCAAT TTTATGAGCA AGTGAAAAAC AACCCCTTCAG CCCAGCNAGT	360
CTTGTAAAT ATGACCATCC AAAAAGTTTT TGAAAAAAC ATATGGCTCA GAGCTTGATG	420
ATAAAGAGGT TGATGATACT ATTGCCGAAG A	451

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

CTATGGATAA GGCAC TTGCT GACCTCA AAAA CATCAGGGCA CTTGCC TATT CCGGCACACC	60
TACGTGATGG GCACTACANT GGAAGCAAGG AACTGGGAA TGCCCAAGAC TATCTCTATC	120
CACACA ACTA TCCTGNAAAT TGGGTCAAGC AAGACTATCT GCCACAAAAA ATTCTGAATC	180
ATCACTATT CCAAGCAGAA TATACTGGTA AATATGAACG GGCTTGGCT CAAAGAAAGG	240
AAGCTATCGA CCATTTGCCA AAAATCTGAA ATCCCTTTCA AAAAATTGCA CTTTCCTCTT	300
GATTTTTTTT GAAAAGTGG TATCATATAA ATATAGAAC GCTGTGGTGT ACCACTTCAC	360
ACTTAAGTGT TGACCGACTA TTTTTTGAT TATTANGGAA ACAAAAGTCT TCTGTCAGCA	420
TGTAGGCCGT CTCACACGGAA AACAGCTTCA GTT	453

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

CCGTAGTACA GGCACAAAAA GATTTGGAAA ATAGAAAAAG AAAAGCCAAG AAAAAGGCTC	60
AGAAAACGAA ATAAAATAAGG AGGAATCTGG TAATGGTAGT ATTTACAGGT TCAACTGTTG	120
AAGAAGCAAT CCAGAAAGGA TTGAAAGAAT TAGATATTCC AAGAATGAAG GCTCATATCA	180
AAGTCATTTC TAGGGAGAAA AAAGGCTTTC TTGGTCTATT TGGTAAAAAA CCAGCCCAAG	240
TGGATATTGA AGCGATTAGT GAAACGACTG TTGTCAAAGC AAATCAACAG GTAGTAAAAG	300
GCGTTCCGAA AAAAATCAAT GATTTGAACG AGCCTGTGAA GACGGTTAGT GTAAGAAACC	360
GTTGACCTTG GTCATGTGGT TGATGCTATT AAAAATAG AGGAAGAAGG TCAAGGTATT	420
TCTGATGAAG TC	432

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

AAAATCAAGA AATTCTTTGA AGGAACGACA GATAACAGCTG AGAAACTATAT CAAAGTCGGCC	60
CTTAAAATGT TGGTCAAATA GGAGCAGAGA ATGACAAAAC GTTGTTCGTG GGTCAAGATG	120
ACCAACCCGC TCTACATCGC CTATCATGAT GAGGAGTGGG GTCAGCCCCCT CCATGATGAC	180
CAAGCATTGT TTGAGTTGTT GTGTATGGAA ACCTATCAGG CAGGCCTGTC TTGGGAAACG	240
GTACTCAACA AACGCCAACG TTTCCGAGAA GCCTTTCCAT AGCTATCAAAT TTCACTCCAG	300
TCGCAGAGAT GACTGACACT GAATTGGAAG CCATGCCTGG AGAATCCCAG CTATCATTCC	360
GAAATAGAGC CCAAGATTTC TGCTACACGC CGCCTAACGC CCCAACCCCT TCCTACAGTT	420
ACAGGCAG	428

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

CTATTAGATG GTATTGACTG CCCAGACACT TACGGATCTA GCTGAGACAG GGAATTGTCC	60
ATAACCTTCC TCATCAATTG TAACTTGACC TTGGTGGTTA CCAAGTAAT CTACAAAGGT	120
TTGATTAGTC CATTCTTGAC CGACAAACAT TGACTTGCTG TTTTCTTGGT CATTGAAAT	180
CAAGACTGCG ATTGGGGATT GATTTTCAGC ACCTGAACGT ACCCAACCAG TACAGTTAGC	240
ATGGTCAAAG TAGTCATTTC GTTCTCCATA GGCCAAATCT TTTCGGATGG CTAGGAGGCG	300
GTCAAGGATT TCTTTGAAAT CTTGTTGAGC ATACTGGCCT GAAATCCCAG AGTAGTCTCC	360
GTAAAAGACA CATGGAAGGC CGTCTTGGCG TAACAAAATG AGGGCATAGG CTGCTGGCTT	420
GAACCATTCT TCAACGGTAG ACTCAAGGGC TTGTCCTCGT TGGGTATCGT GGTTGTCGAC	480
AAAATCACAG ACTTGTCAAGG CTTGAGTTCA ACCAGGCT	518

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

CTCTGTCCTT TTACCTGAGA GTTTGAGCAG TTGCCTGCCT TGCCCCCTCG GTGCCCTTAC	60
GGTCTCTCCA GAGTTCCGTC CATTACAGT CATGGAAAAT CAAACGATTC CCCACTTCTA	120
TTAAACTTCA TTCGGTGTTG GTATTTAATT GATTCTAATT TTACAAAAAA TGTTGGCTTT	180
TGTCAATGTG TTTATTAGTA AAAATTAGTT CAACAGTTTT TACTTTATAA AGTCCAGAAT	240
ACTGCTATCC TTTAAAAGTG ACAATAGTCG CACCACTGCG TCCAGCATTT TGTTGGGCAT	300
AGCCGAAACT CTTGACATGT TTGTTTCTTT GCAAGTATTG GGTAACTCCT TCACGGATGA	360
CTCCTGTTCC GATACCATGG ATGATATCAA CTTGAGCCAT ATTGTTAACG AAGGCTTGGT	420
CGAATGAAGG TATCTAGCTC ATTCAATGGCT TCTTCATAGC GCTTGCCTCG AAGATTCACT	480
CTAGCTTGAG TCCTCGCCCA GAAGTTCG	508

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

CTCTTGGGCT CTCTTCTCAG CAACTCCCT GCTTTCACCT TTGGTCTTGA TAGGTGANAA	60
CGTAAATATNT CCAATCNNG TCATATTAGG AAANAGTTAA ATTGTTGGAA AACCATGCC	120
ATCTTCTCAC GCATGGGAAA CAGGTCATTC TTCTTGTCCG TAATATCGAC TCCCTCAAAG	180
ATAACCTTCC CCTTGGTTGC TTCTTCCAAC AAATTCAAT AGCGAAGCAA GGTAGATTT	240
CCACTCCCTG AAGGACCGAT GATAACGACA ACTTCTCCTC TTTTAATCTC GAGGTTGATG	300
CCCTTCAATA CTTCATTCTT TCCAAAAGAT TTATGTAATT TTCAATTGTTT ATCAAGGTTT	360
CTGTCATTAT TTCTTATC	378

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 741 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

CTGGCCAGCC AGATAAACCT CGATACGGCT TTCTGCTCGT TTGATGCCGT GCAAGAGTCC	60
GCCCATAACGG ACGTCAACTG TATCCAAACC AAAGACCTTG TTTTATTTCGA GCCAGTGGTG	120
ACTAAAGAGG GCATGGAAGT CTTCAATTG GCTTCTAAGT TCTGGTAATT CTTGCTGGC	180
GATTGTTGT AAACTTCTT TATCATCCGC TTGGTAGGC TGACGAATGC GTCGTCCCAC	240
ATCTACTTTG CTACTTAAAA TAGCATTCAA CTGGGCCTGA GTTTCAAAGA GATAAGCATA	300
GTTTCCAGCT TTTCTTTAA TGTCAGCAAT AGTTCCCAGC GCCTGAGCGA AGTGTGGCTT	360
GTCCTGTTCA GGTGTCAATGT GTCGGTCAAG TATCGGACAG AGAACATCCT GATAAAAGAC	420
ATAGCGGTTG GGATTGATGC CACTGAGATT ACCTGGTAGG TCTGGTAAGA GGTTGGCAAG	480
ATCAATCTGC ATAAAATCCT CAACCGTTAG ACCAGTATTG GTCTGAAAT GCGCAGACAA	540
ACTATCTAGG TCATTGCGAT AGATCAAGTT ATCGATACCG TCGACCTCGA GGGGGGCCGT	600
ACCCAGATTT GCAAGCTTGG TAGGATAAAAG AACTGGGCAG TTTCACCAACC ATTGTCTCCC	660
CAACCCGTTA CGATGACTTC TTTAATCTGA TTGGCACGGC AGGCTTTATT AGCCTCGATA	720
GCCACTAGAC GGCTAAAATG G	741

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

AAACTCGATT TGAGAGAAAG TCCAATAAGT CTTTCCATAA TAAAACGCAT AGTAGCAAGA	60
GTTTCTACAC CCACTATTAT GCGTTTTAT CATTGGAAA TCTACTGCTA ATCAATGAAG	120
AAGCAAAGAT CAAACTAGGC AGCTAGTTAC AAGTTACGTA AGCGCGTCAT AACAAAGGTAT	180
CTATCCTAAT TCCCCAACTT CCAGTACTAG AGATAAAAAAA TAATTATCGG AGGAAAGGTA	240
TTGTACTATG ATAATTCAAC TAAGTGGATT AGGTCAAGTT CACCTTGTGTT GTGGCAAGAC	300
AGATATGAGG CAGGGAAATAG ACTCATTAGC CTATGTAGTT AAAACCCACT TTGAATTGGA	360
TCCCTTCTCC GGTCAAGCCT TTCTCTTTG TGGTGGACGT AAAGACCGCT TTAAAGCCCT	420
TTACTGGGAT GGTCAAGGAT TTTGGCTACT ATATAAACGC TTTGAGAACG GAAAACGTAC	480
TTGACCAAGT ACAGAAAAGG ATGTCAAAGC TCTCACACCA GAACAAGTAG ACTGGCTTAT	540
GAAGGGCTTT TCTATCACTC CCCAAATATA GTGGATTAA ACTAGAAATAG TACACCCCTA	600
CTTCTAAAAC ATTGTTAGAA ATCGATTGTA CTGTCTGAT CAATTGTCG TTGTTCTTATT	660
TCATTTTACT ATAGAATCCA TCTGAAAGCC GTTTATGATT TCTATTGAAA TGAAGACCGT	720
CCATTTTAGT AGACTAAAGG ATTACTCAAACCTTCAAGA GGAAGACAGA TGAACCTGTT	780
TCTTATAAAA ATGTTGTCTG AAACATATTGCTTCTTCCAA GAAATTGAG AGGAAGAAAA	840
CTTTATGAGG AAAAAGGAGT TACTCAAATA ACAATTCAAGG ATTAAAAATA GACAGTTGAG	900
GAGCGGAAGG TATAAATTAA GTTTGCTACT GTATAATGGA TTTAAATCAC TCACCGACACA	960
GAACGAATAC TCTTCGAAAAA TCTCTCAAAC CACGTCAAGC TTGCGCTTGC CGTAGATCCA	1020

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TAGGGGACTG GACTTCATCA GTTCTATCAA CAACCTCAA ACAGTGTTC GAGCTGACTT	1080
CGATCAATT TATCTGCACC TCAAAGCTGT ACTTTGAGCA AGCCTGACGA CTAGCTTCCT	1140
ATTGATTTT CATTGAATAT CAGAAACTCA TTCTCCATCA AATAATCGA CTGGTCTAA	1200
TAATTTTG TCTGGCACGG TGTAGAAAT AAAGGTTGTG TATTTGGAGA GGGGATTAAT	1260
TTAAAAAAAT CCAGTCTTGT AAAATTAGA ACTATCAATC AGTAAGATGG TTTCATGGC	1320
TTTGTCAATA ATATTCTTT TTGAAATAG	1349

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

CTTTTTTATA AGCAATTCAA TTTTATACTC ATCTGCTTTC AAAAGCATT CTAGTCCATC	60
TCCGATTAAC GATGGACTTT ATCACCTCCT TCTCCAATCC TTGTATGACA TCTTGAAGTT	120
GATTCAATGAC ATCTTCCAAA ATTGAAAGG CTTTATTCTT AAATCCACGT TTACGAATCT	180
CTTTCCACAC TTGTTCAATG GGGTCATCT CTGGTGTGTA TGGAGGAATA AATGCAAAC	240
CAATATTAGT CGGAATCTT AAGACACTTG ATTATGCCA TATAGCATTG TCCATAACGA	300
GTAAAAAATA ATCATCTGGA TAAGCTTGTG AAAGCTCTTC TAAAAAGGCG TTCATCCACT	360
CAGTATTACA TCTACCAGCT ATTAAGAAAA AATGATTCCG CCTGTTATGG GCATCAACAG	420
CTCCATAACA ATAGTGAAT TCTCGTATAT AGTGACTATG GACATGTGGA CCTACTCCTA	480
TTGGAGACCA ACAAGATCCC AGTTTACTGA TTCTACCGAA ACCAGCCTCA TCTTGGTACA	540
TCAAGCGAAC CTTATGAAAA CGTCTACTGG TTAAATCGC TTTCTTGTCT TCTTGAATTG	600
AGATTTTATT TTTAGACGCG ACAATGGTTT GAGCGTCTGC TTTCTTAGGA TGTTCTGGAC	660
GTGGCATAAT ATTCGCCAG CCATGGCGCT TCAACAGTTG ATAGAAGGCA TCACGTGTGT	720
AGGAACGACC TAACTCCTT TTATAAGCCT GAAATAAGGC ATCAATTGTA ACAAAATTCTC	780
CTGCCTCTGT AGCCTTCAA TGGCGGCAA GAAATACTTT CTCTTCTCA ACTGTCATAT	840
ATGCATGGTT ACACCACCA TTTCTGATA GAGTTGTTCA CATCTTATT CAAACTACTA	900
TAAAAGTTCT ATAATCTCTT TATAAGATTT GCCCATCAGA CGAAATATAA TAAATTGAAA	960
CTAGAATAGT ACACCTCTAC TTCTAAACCA TTGTTAGAAA TCGATTGAC TGTCTGATC	1020
GATTTGCCCT ATTCTTGTCTT CGTTTACTA TAGAACGATT TGAAGGCCTT TATGATATTG	1080
AGCTGTACGA GAGTCTTTTA AAAGTGTGTT GATGGCTTGG ATTTCTTCTT TAGTTGATTT	1140
CATATCACTA TTATATAATG CTTTTGATC TTAGTTTAG TATTATCGTA GAAAATGGAC	1200
TAGGTGCTAT GGATACACCG GATGAGAATG GTTATGTAGC AGATGACTAT CGGATTACTT	1260
ACTTAGAGGC CCACATCAAG GCCATGCGAG ATGCCATTAA CCNAGACGGG GTTGACTTGC	1320
TTGGTTATAC GACTTGGGGC TGTATCGATC CAGTTCAG	1359

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

CTAGTATTTC CGTTGTGNNTT AGTTTGTCTG CCTATGGAGT TATTGCCTAT GTGCAAGGTC	60
AGNTGGATAT TCTTCTAGTG ATTCTGGCCA TGATTGGTGG TTTGCTCAGT TTCTTCATCT	120
TTAACCATAA GCCTGCTAAG ATCTTATGG GTGATGTGGG AAGTTTGGCT TTAGGTGGAA	180
TGCTGGCAGC TATCTCTATG GCTCTCCACC AAGAATGGAC TCTCTTGATT ATCGGAATTG	240
TGTATGTTT TGAAACAACT TCTGTTATGA TGCAAGTCAG TTATTTCAAA CTGACAGGTG	300
GTAAACGTAT TTTCCGTATG ACGCCGTGAC ATCACCAATT TGAGCTTGGG GGATTGTCTG	360
GTAAAGAAA TCCTTGGAGC GAGTGGAAAGG TTGACTTCTT CTTTGGGGA GTTGGGCTTC	420
TAGCAAGTCT CCTGACCCCTA GCAATTATTT ATTGTATGTA AGAATGGCAC CCTGATGTTT	480
TAGGGTGTAA TTGTGTTAA ATACACAATG AAAATCAAAG AACAAACTAG AAAGCTAACT	540
TTAGGCTGCT CAAAACATAG TATATTGAAA CTAAAATAGT ACACCTCTAC TTCTAAAACA	600
TTGTTAGAAA TCGATTTGAC TGTCTGATT ACGATTATC CTGTTCTTAT TTCATTTTAC	660
TATACCATCA ATAAGTGTG AAAAGATCGT TGACAGAACT GACCAAGCCA GATCATCTTT	720
GTAACCACCT TGAGCTTGTG GCATATTGT TAATTGAGCA AAGGCCTAG AAGAGTTGC	780
TGGGTCAAGCA GTTGCAGATT TTCCTTTAG TTCAGGTTG AGAAGGTCCG TATATCCTTC	840
GATGTTCATG CCTTTAGTTA AATCAGGGTG GACGATTAAA ACACCTACCAT CTAGTGTATA	900
AGGAGTAGAG AAGCCAGTTG TGTTTTGATA TTCTTTGATA ACATTATCAT TTTCTTTGAA	960
AATATAGTTT TCAAAGAGTT CTCCGTGGGT AGCATATTGT GTTATAAGAA CCACCAAAGA	1020
TAACATCAGC TACAGGAAC TCTTTTCTG ACCTAGTTT TTGAAAAGTT CTCCAGTACC	1080
AG	1082

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS.

- (A) LENGTH: 1303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

CTGGACTTGA TAGGCATCTT TGTAATCCTC TAAAGCCTCT TTCATCAAGG CACTACCAAT	60
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TCCTTGACGC	TGATAGATTG	GTAAAACGAT	TAAATCCTGA	ACCAATACTG	ATGAGAATCC	120
ATCTCCAACC	AAACGAATCA	AGCCCACCA	AGCATCACCA	TCAAGTGCCA	CATAAATTAC	180
TAATGAATGA	GATAAGGCCT	GCTCCAGCAT	CTCTGGTTGA	TGGGTATAAT	TAGTCCAACC	240
GACAGCCTGA	TAGACATGTA	AAACATCCTC	TAGCTTGACA	ATTTCTTGCT	TTTTAATAGT	300
AATCATCTCA	ACACCTCTTA	AAGTCTCTC	AAGCTCTTGT	ACTGCTGTCC	ATTTTTATCA	360
AAATTTTCAG	GACGCCAACCA	TGTTTCCAAA	CGATCTTGA	CTTGGGCCA	GTCCTTATCA	420
ATCATAGACA	ACCAATCCAT	ATCTCTCGTA	CGCCCCCTTAT	AAACCACACTGC	CTGACGGAAG	480
GTTCCCTTCAT	AAATAAAGCC	CAAACGCTCC	GCAGCACGTC	TGGATGGCAG	GTAAAGAGCA	540
TCGCATTCC	ACTCATAACG	ACGATAGTTA	AGCTCTTCAA	AGACATAGCG	AGCCAGTAGA	600
TACTGGGCTT	CTGTCCCTAT	CCGTGTCCCC	CTGAGTTTG	GAGAAAAAGT	GACAGCTCCC	660
ACTTCTATT	CTCCGTTACT	GGTCAATACG	CATGAGAGAA	AAATTCCCAA	AGCCTTACCA	720
GTTGCCCTGT	CTATGTAGTA	AAAACGGTCC	TTACGAGCCA	ACATCTGACT	ACTATAGTAG	780
ATTGAAACTA	GAATAATATA	CCTCTACTTC	AAAAATATTG	TTAGAAATCG	ATTTGACTTC	840
CCTGATCGAT	TCGTCCATT	CTTATTTCAT	TTAATATATAA	TTGATAGTGG	TCGCCCCAGC	900
CAGATACCTT	ATCTGCTATC	CATTTAGGAA	CCCCTAACTT	AAGCAATCCC	CATAATCGTC	960
TCGATTTCTT	CTTCCATTGC	TTCCAGATAA	TCACTCGTAG	GCGAGTACGC	AAGCGCTCAT	1020
CTATGTTAGT	GACTATACTT	TTCATATTTA	TAATTCAATT	CTTTCGTTTC	ACTCAAGGCA	1080
CAACACAGAA	TGAAAAAAGTG	TTGTGATCTT	TATTTTGTTT	TATAATAATA	GTGAGAAAGC	1140
CTATCACTAC	TACAAATCAC	GGGGAGGTGA	ATAAGTGAGT	GGTACAGCCA	CTACCTCGCA	1200
TATMMTGTCA	CATCATTAA	CGGTACATAA	TAAGTTGTAC	CATCTGAATA	AGTTGCTACA	1260
ATATCATTG	CATGCTCTCC	TTCACCTTTA	GCAAAGGTTG	GAG		1303

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

CTCTTCAATC	AACTCACGCT	TTAGGGCTTC	CTGATGATTT	TCACCTGCTT	CAATTCTCC	60
ACATGGTAGG	AACCAAGCAC	CATTTGGTT	TTGAACAAAGA	ACAATTTGTT	TTTGTTCAGG	120
ATTAGGGATA	ACTGCATATA	CGCCATAGCG	AGCAATATAG	TCTGTATTG	CTTTTTCTC	180
CGAAAGTTGG	GTGTCGCATT	GCATTTCT	CATTATCTAG	TATCGTTATT	ATTATAGTGA	240
AATGAACCAA	AAATAGTACA	CAATGTGGTA	TAATCTTTT	ATGGCATATT	CAATAGATTT	300
TCGTAAALAA	GTTCTCTCTT	ATTGTGAGCG	AACAGGTAGT	ATAACAGAAG	CATCACACGT	360
TTTCCAATC	TCACGTAATA	CCATTTATGG	CTGGTTAAAG	CTAAAAGAGA	AAACAGGAGA	420
GCTAAACCAC	CAAGTAAAG	GAACAAAACC	AAGAAAAGTT	GATAGAGATA	GACTAAAAAA	480
CTATCTTACT	GACAATCCAG	ACGCTTATT	GACTGAAATA	GCTTCTGAAT	TTGGCTGTCA	540
TCCAACCTACC	ATCCACTATG	CACTCAAAGC	TATGGGCTAC	ACTCGAAAAA	AAGAACCCACA	600

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CCTACTATGA ACAAGACCCA GAAAAAGTAG CCTTATTTCT TAAGAATTAA ANTAGTTAA	660
AGCACCTAGC ACAGGTCTAA CAAATGGTGA ATTAATCGCT CCAATGACTT ACGAAGAGAT	720
GATGACGAGC GACTTTTTG AAGTATGGTT TCAGAAGTTT CTCTTACCAA CATTAACCAC	780
ACCATCGGTT ATTATAGTGA AATGAAATAA GAACAGGACN AATCGATCAG GACAGTAAAA	840
TCGAATTCTA ACAATGTTT AGAAGTAGAG GTGTACTATT CTAGTTCAA TCTACTATAT	900
TAATGGACAA TGCAAGATTC CATAGAATGG GTAAGCTAGA GTTCTTATGT GAAGAGTTG	960
GGCATAAACT TTTACCTTT CCTCCCTACT CATCTTAGTA TAGAAAAGTG AATCTAAAAT	1020
AGTACATAAC TGCTTCTAAA ACATTCTTAT AAATTGATTT AAATTCTCAA ATCATATTAT	1080
TCAGTTCTTA TTTCATTTTG CTCTACAATC CTGTTGAGAA GACACGTGTT CATATCAAA	1140
AGGTATTGGC AAGTTGCAAT ACCTTTTAC AAGGTTCTTT TGTCTTATTT TTGTTCAAC	1200
TGACTATATC TCCTATGGTT CTAGTCAGA AGGCTAGGCT ATAATTATGA TTGATAAGAA	1260
GTATCATTCC AAGTATTGAG AGTGAATGTT TCAAAATCAT GGTTTCTAT AATGGTCAGG	1320
CTGGCATTG CTAGACCGCC ATCTTACGA AGAAGTGGTT CTTTATAGCC TAGGAGAGTA	1380
CGAACACTGG CAGTAAGATT GGCGCCGTGT CCGACAATTA GAATACGCTC AGCTGGACTA	1440
TCTTTTAATG ATTTGATAAA TTGGATGGTC CGCTGAGTTG TACTATAGAG GGATTCGGCT	1500
CCGAACATTC GAGTGTCAAA TTGAGCAAGA TTTGAACGAA AAGCCTGGAT TTGTTGCGGG	1560
TAAATAG	1567

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

CTGTTCCAT AGCATGACTT CTGTACTAGA CTTCTTTTC CGAATAAATA GATAGAACCA	60
CAGAACCTAG TAAACCTAGA ATTAAAAATTAA TGGTATAATA TTAGCAATAA AAGAAATCTG	120
GAGGATTAGA ATCATGGTAT CAACGAAAC ACAAAATTGCT GGTTTGAGT TTGACAATTG	180
CTTGATGAAT GCAGCAGGTG TGGCTTGTAT GACGATAGAG GAGTTAGAAG AGGTCAAAAA	240
CTCAGCGGCA GGAACCTTTG TTACTAAGAC AGCGACCTTG GACTTCCGTC AGGGGAATCC	300
TGAGCCACGC TACCAAGATG TTCCACTTGG TTCCATCAAC TCTATGGGCT TGCCAAATAA	360
TGGCTTAGAC TATTATTTGG ATTATCTTT AGATTTGCAG GAAAAAGAGT CGAACCGAAC	420
TTTCTTCTTA TCTCTGGTCG GCATGTCTCC AGAGAAACCC ATACTATTT GAAAAAGTC	480
CAGAGA	486

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CTCTATCAGG AAAGTTAAAT TAATTTATAG AAATATTTA GTATTTAAGC CCTACTGTGA	60
TAGATTCAAT ACACATATA TGTGTTGTC TGATAAAAAT TTCTACTCTT TTTGATTTA	120
AATAAGTATT AGTTTACATT ATGGTGTGAA TTGGGTTGA TATCTCTTT GAGGAAGTTG	180
CCTTAGATTT TTCTGATTGT GTTTATTGT ACAGTGTATC TTGCTTGTGTT TGAACAGAAC	240
TTTTATGAC ATTTGTCATA TTTTCTAGTG ACAGAAGCTT CTGCCTCCCT TGATTTAAA	300
AGACTATAAT TGTAGTATGA AATGGGGAA GAAGAGATGA GAAATAAAAT GATTATCGCA	360
GTAAGTTAG TAGTAGCAGG AGTTATGACC TATCTCATGT TTTGGGATT GGATGAGAAC	420
TTCTACCATT TTCCTGGGA GGTCTTGCT GGCTTGGAA TCATCTCTT GGCTTGTCCA	480
GAGAAGGTTT GAAATTAGTA AGAGATGTGA AAAAGGAGTT TGAAAAATGA AAAAAGCAAC	540
TATCTATTTT TTTATCGGCC TGTCACTCTT GGTATGGTTG GTAGAAATGT TTACAGGTTG	600
GTTTGCTCAA ACCTTCCCTTC ACCAGTTCAT CGTGGTGCA TGGGGATTAG GATTATGAT	660
TTTTATGCC TTTCCGATGG GAAAGGAGTT GCTGGAAGGA GAATATCATG AACATGATTA	720
AGGTTCAAGG ACTACATAAA AATATTAAGG GCAAGGCTAT TTCAAAGGAT ATTCCTTGT	780
AAGTAGCAGA AGGTGAATGC GTTGCCTGAA TTGG	814

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

CTTGGTACGA CCGTATGGGT GGTCACTGAA AGTGGGAAAC TTCCAAGATG GGCACTGTGT	60
ACGGATCCCC GTAAACTGTC GCANAAGAAC TGAAGATGAT GTTTTACAG TTGTTTCTT	120
CCATGGCTTT CAAAAGGCTG ACAGTCCAG CGATATTGTT GTCATAGTAG GCAAGAGGGA	180
TACGTGTTGA TTCGCCAACA GCCTCAAAAC CAGCAAAGTG AATGACACCA GTCAGTTCTT	240
CCTGTTGAA AATATCTCTG AGGGTATCTG TGTCACNAAT ATCTGCCCTCA TAGAAAGGAA	300
TCTCAACTCC TGTGATTCTT TCAACAACCTT CTAAACTCTT ACNATTGCTA TTGACAAGAT	360
TATCCACAC AACAACTTGA TGGCCTGCTT GGATCAATTG AATAACAGTG TGGGTTCCAA	420
TAAAACCGGC ACCACCAAGTT ACCAAAATCT TTTCTTGAT CTTTTTCCCT CGATTCTCAG	480
ATTATTTTTT CTTATTTAA CCATTTGAA CAGGAAATGT CATTGCCCAC CTTAAACTAC	540

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CTGATAAAAT TTCAAGTAAAA TGCTTATACT CTTGGAAAAT CCAATTCAAAC CCACGTCAAC	600
GTCGCCCTTGC CATGGGTATG GTTAAGTGACT TCGTCAGTTC TATCCACAAAC CTCAAAGCAG	660
CGCTTTGAGT AACCCGCGGC TAGTTTCNTA GTTTGGTCTT TGATTTCAT TGAGTATTAT	720
TCGCTTTTA CTCGTTGAC ATAGTTTCA ATTGGGTAGT TTTCAGGGTC CAAGGTCAAC	780
TCCCTGTCTT GGATCAGTTG AGCTAAATGG TAACCAATAA TAGGACCAGT TGTGAGGCCT	840
GATGAACCTA GTCCACTGGC TGCAAGACA CCAGTTAAGT CAGGCACCTG CCCAAAGAAA	900
GGAGAGAAAAT CACTGGTGTG GCCACGGATT CCAACACGCT CAGATTTGA AGTAGCTTCA	960
GCCAAAATCA GATAGTGAGT CAAGGGGCC TCCTCCATTG TTGGAGCAA GGTTTCATCT	1020
ACCGTCAAAT CAAATCCCCT GTCATTTTCG TGGTAGCGC CTAAGGACAA TTTCCCACCT	1080
GCAAAAGGAA TCAAATCCCA CTCCCCTTCT GGCAATGACAA CAGGGTAAGC TTCCATGTCT	1140
TGGACCAGCT GATAATCTCG TAGTTGTCTT TMTTGAGGAC GAACATCTAC TTCATAACCC	1200
AAGGGTTCTA ACATGTCCCC CAACCAAGCT CCNGTCGCCA AAATAACCTG CTCAAACTCC	1260
TCTTCACCAA TCTGGTAGCC TGATGCTAAC GGTGTCAGAG TCACCTTTTC TMTGACCAG	1319

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

CTCAAAATAC TGTTTGAGG TTGCAGATGG AAGCTGACGC GGTTTAAAGA GATTTTCGAA	60
GAGTATAAAC TGCTTATAAA ATAAAAAGGA GCCCTGATGG AACACATTAT TTATCAGTTT	120
GAAGAGGACT TGGCAATCCT TACCTTGAAC CGTCCTGAGG TCGAAATGG TTTTCATATT	180
CCCATGTGTG AGGAGATTTT AGAAGCTCTG ACTTTGGCAG AAGAAAATCC AGCTGTGCAT	240
TTTATCTTAA TCAATGCCAA TGGAAAGGTC TTCTCAGTTG GGGGAGATTT GGTAGAGATG	300
AAGCGGGCAG TGGATGAGGA TGATATTCCA TCATTGACAA AAATCGCAGA GTTGGTCAAT	360
ACGATTCTT ATAAAATCAA GCAAATAGCC AAACCTGTTT TTAATGGAAG TTGACGGTGC	420
TGTTGCAGGT GCCGCAGCGA ATATGGCTGT TGCGCAGAT TTCTGTTGG CGACGGATAA	480
GGCTAAGTTT ATCCAAGCC CTTTGTGAGT GTGGTTGGCT CCAGATTCCA GGGG	534

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 784 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

CTGCAGCCGG AAGTTATCTG GTTACAAAAA ATGCCAAC CATCACAGAT GAAAGTCCTG	60
AATACCACTG ACCCGCTTCA AGCTATCAAG GACGATGTGG ATATTATCCA AAACAGCCTG	120
CAAATCATTA ACCAGAAAA AGAACTTATC AAGGAATACC AAGAAGACTT GACTTACAAG	180
TTTAAGGTCT TGGAAAAGGA TATCCAAACT AGGACTAGCT GTGATAAAAG AAATGCAGGG	240
AACTGAAGAT AAGTAAAAAG AGCCCGACGG CTCTTTTTA AAACGTAAAC AACTTATAGT	300
GAATTGAATT TAGAATAGCA CATCATAGTT TCTAAAGCAT TGTTAGAGAT TACTTTAAAA	360
TCCTCTTATC AATTGTTCA TATTCTATTT CAATCTACTA TATATATCCC ATCAACTATG	420
CATCATAATT TAGGTAACTC ATACTCAATA AAAATCAAAA AGCAAACCTAG AAAGCTAGGC	480
ACAGACTGCT CAAAACACCG TTTAAGGTT GTGGATAGAA CTGACGAAGT CAGTAACCAT	540
ACCCATGACA AGCCGACGCT GACGTGGTTT GAAGAAAATT TTGAAGAGTA TCATTCACCA	600
TTTCACAACAA AAATCGAAGA CTTCTGCCG TAATGAAAAC ACCTGAAACA GCTTGGTTTC	660
AGCTGTCCGG AAACTTTAAG ACTTAGGTTC AAAGTTTAGG TATGGAACCT CGAAGGAGGT	720
CGCTACCGTC CGTCATTACT TAGNGAAGNC TTAAAAAATC TATAAAGTAA AAAGAGCCCCG	780
ACAG	784

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

CTACTCGTT TAGTATAGTA AACTGAATCT AGACTAGCAC AATGCNGCTT CTANAGCGTT	60
TCGAAACTAG AATAGGACAA CATAACTGCT AAAAGATTTC TATAAAATCA TTTGATTTTC	120
CTAATCAATT TGTCGTATC CTANTTCACT CCACTATAAA ATATTCTTAT CAATTGATTT	180
GNATGCCAAA ATTCCATCGT TCAGGTCTTA TTTCATTNGG CTNTAAAAAA CTCTCCTGGG	240
NAATCCCAGG AGAGNATGAT TACNTATTG AACTTGAATC CPTCGTANAT AAGCTCTGTT	300
TTTGGATTT GTTTCTTAAT CTGTTGGCA AGTGCCTTC A TCATAGAAAT AGGACCACAC	360
ATATAGACGG TTGCATGTTG GGGCACTTTT TTTGTTCAAA ATTAAGATAG CCGTCTTTCG	420
TACTGTCGAT TAGATGGAGT TCAAAATAG GATTTTCTG ACCATAGTTA CGGAGTAAAT	480
CTAGGTAGAC TGCATTTCA TCTCCACGGA AGCTATAGTA GAAAGTGAACC TGTTTATCTA	540
AAATAGGATG TTCACGGATG TAAGAGATGA AGGGGGTGAT CCCAATACCT CCAGCAATCC	600
AAACCTGATT TTCTCGTCCT TCTTCTATGA TCATGTGTCC GTAAGCTCTG TCTAGGGTTA	660
CTTGTGCTGCC GGCTTGAAGA TTATCATAGA TATTTCTTGG TATGGTCCCG TGAATTTTA	720
ACAGTAAAGT TAAAGAGTTT GAACCCATGA ACTCCCTGAG AATAGAAAAG GGATGCCGGA	780

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ACCACTTCA AAGCCTCTT GGAAAATCTT TAGAAAGGCA AATTGTCCTG ATTGATAGTT	840
GAAAGGTCTG CTAAGATGGA TTTGAATTTC TCTAGTATCG TGATTTAACG GTTTGAGATG	900
GGTAATTTTC CCTAGATAGG GGAAGGAAAT CTTTGATAT AGAAAAATGA TATAAAAACC	960
AG	962

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 910 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

CTCTTTCCAC TATTATAACA CGAAAGAAAG AATTGTCAGG GAACTGTACA GATTTCTTTT	60
CTATCTATTT ATAACCTCAAT GAAAATCAAA GAGCAAACCA GGAAACTAGC CGCAGGCTGT	120
AATTGAGTAC GGCAAGGCAGA CGITGACCGCG ATTGAAATTG GATTTTCGCA GAGTATTATT	180
CGTAAAAAAT CTCAAAAAGC CTACCTTCG GTAGACTTAG TTTGTTTCTA TTCTAATCGG	240
CACTCTTCCA AAATTTTGCT CTGCTATACT TGGCTTCCT AGTTGGTAAA TCTGGTCAAC	300
CTTTTGAGTC ATAGCATCCC AAGGTTCTTT GCCAATTCCG CTGACTAGAT TGACCTGTCC	360
TTTCAGAGAC TTGAGATGTT GCCTGCCCTT TTCAGTAAAT CCAAGGACAT GAATGGCTTC	420
TGGCAAGTCA CTTTCTCTAG CCTGCATCAA AATATAGGTC AATAGGCGTC TGACACGCGC	480
CTTGGTGTAA CGTTGGTAG TCACTAACTC GACCAATTCT TCCACAGACT GGGCTGTTTT	540
AATAGCTTCT TTAATGCGCA CAGCCATTTC TTGATTGACC TGATAGATGG TGGTTAGGTC	600
GGGATTGAC AAGATTTGAT AGCGGAGCAA GGGAAAATAG TCTTCCCAGA TCACCTTACT	660
GGCTTGCTCA AATAGGGCAA CAGAAGGCAT AAAACGTTCT AAGAAATCTT GGTCTTCTG	720
ATGTTGACGG AGGGCTGTAG CCGAGGCAA GTCCACATCT TTATTACAG AATGGTAACC	780
TGCCCCCTGA CGCTGAATCG GATGCAGCTT GATATTCCGT CCTGCAACCG CCTTGGCATA	840
GGCCAAAACA AAGAACATGA TTGGGGTGTAA TTACCTGAAA AATCAAGACC AGCAAATTCC	900
TTCCACATAG	910

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 866 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

CGCCAAGTCA	TCCAACAAGT	CCAGAACGGT	TCTGGGCTT	GGGATCCTCA	GTCGCTGGAG	60
ATAACTCCTT	TGGGCTTGTT	CATCATGTAG	TAGACAAACT	CTTCATACTC	CAACACTTGC	120
CCATCAAAG	CGAATCTCAT	CTATTTTTC	ATCAATCTGC	AATTTAGCTG	ATTTTCTTT	180
TTTACCATT	ACAGTCACGC	GCCCAGCCTT	GAGCAAGTTT	TTGACCTCAG	TCCGACTTCC	240
CACCGCACAG	GCAACTAAAA	ATTTATCTAA	TCTCATAGAA	CTATTATATC	ATATCAAAG	300
GAGGCTGGTA	CAATGACCAA	CCTCCTTTTC	GTTCATACT	CTTCAAAAT	CTCTTCAAAC	360
CGCGTCAACG	TGCGCTTGCC	GTATATATGT	TACTGACTTC	GTCAGTTCTA	TCTGCAACCT	420
CAAAGCAGTG	CTTGAGCAA	CCTGCGGCTA	GTTCCTAGT	TTGCTCTTG	ATTTTATTG	480
AGTATCAGAT	TTAGGAAATT	AACTCCTCG	TCTCCAAAAA	ATAGCTAAGA	CAATCATGGC	540
ACCTAAAACA	GCTGGGATAA	TAGCTGTTCC	TGATAAAAAC	GGCCCCAAG	TTCCAAAGAG	600
CAAGTGACCT	AGAAAGGCTC	CGATCCAACC	GAGAAACATT	TTTCCAAAAC	ATCCCATTG	660
CTCTCCACGA	TTGGTCATAG	CACCTGCTAA	AAATCCCAC	AGGAGACCAA	CGAACATACT	720
TCCTAACATA	TTATCTCCTT	AATTGCCCC	ATTCCCATT	CGGAAAAGAA	GTACTCGCGT	780
TCCATCCTCA	CGAATACCAT	CGATATCCAT	TTGGTTAGAA	CCAATCATAA	AGTATACGTG	840
AACATCTGAA	CGGTTAACGCC	CTGCAG				866

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

CTTCAGGATG	TGGGAAAACG	ACCCCTCTTC	GTATGATTGC	AGGTTCAAC	AGTATCAAAG	60
ATGGAGAATT	TTACTTCGAT	GATACAAAAA	TCAATAATAT	GGAAACCCAGC	AAACGCAATA	120
TCGGGCTGGT	TTTCCAAAAC	TACGCTATTT	TCCCACATTT	GAUTGTCGA	GACAACGTTG	180
CTTTTGGTCT	TATGCAAAG	AAGGTTCCAA	AAGAAGAATT	GATTCAACAG	ACCAACAAGT	240
ATCTTGGACT	CATGCAAATT	GCTCAATATG	CGGATCGAA	GCCCATAAA	CTCAGTGGTG	300
GACAACAACA	ACGTGTCAACC	TTGGCATGCG	TCTTAGCGGT	TAATCCAAGT	GTTCTCCTCC	360
ATGGACGAAG	CCACTTAGTA	ATCTGGAGGC	CAAACCTTCG	TTGGATATGC	GTTCAAGCCC	420
ATCCCGAGAA	ATCCAACCAC	GAAGTTGGGG	AATTACAAC	GTTTATGAA	CCCACGACCA	480
AGAAGGAGCC	ATGGCTATTT	CAGACCAAT	TGCCTGTTAT	GAAGATGGG	GTGATCCAAC	540
AAATCGGCCG	ACCAAAAGAA	CTGTATCATA	AACCAGCTAA	TGAGTTAGTG	GCAACCTTTA	600
TCCGGACGCCAC	AAATATTATC	CCTGCCAATC	TTGAAAAACG	GAGCGACGGC	GNTTATATCG	660
TCTNTTCAGA	TGGANANGCC	CTTCGAATGA	TAG			693

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Met	Ser	Met	Phe	Thr	Met	Val	Lys	Met	Asn	Pro	Leu	Arg	Gly	Leu	Ile
1					5						10				15
Cys	Asn	Leu	Lys	Gly	Asn	Lys	Ile	Thr	Ala	Leu	Ile	Gly	Pro	Ser	Gly
						20				25				30	
Ser	Gly	Lys	Ser	Thr	Tyr	Leu	Arg	Ser	Leu	Asn	Arg	Met	Asn	Asp	Thr
					35				40				45		
Ile	Asp	Ile	Ala	Lys	Val	Thr	Gly	Gln	Ile	Leu	Tyr	Arg	Gly	Ile	Asp
					50				55			60			
Val	Asn	Arg	Pro	Glu	Ile	Asn	Val	Tyr	Glu	Met	Arg	Lys	His	Ile	Gly
					65		70			75				80	
Met	Val	Phe	Gln	Arg	Pro	Asn	Pro	Phe	Ala	Lys	Ser	Ile	Tyr	Arg	Asn
						85				90			95		
Ile	Thr	Phe	Ala	His	Glu	Arg	Ala	Gly	Val	Lys	Asp	Lys	Gln	Val	Leu
						100			105			110			
Asp	Glu	Ile	Val	Glu	Thr	Ser	Leu	Ser	Gln	Ala	Ala	Leu	Trp	Asp	Gln
					115			120			125				
Val	Lys	Asp	Asp	Leu	His	Lys	Ser	Ala	Leu	Thr	Leu	Ser	Gly	Gly	Gln
					130		135			140					
Gln	Gln	Arg	Leu	Cys	Ile	Ala	Arg	Ala	Ile	Ser	Val	Lys	Pro	Asp	Ile
					145		150			155			160		
Leu	Leu	Met	Asp	Glu	Pro	Ser	Leu	Ser	Leu	Gly	Ser	Asp	Cys	Asp	His
						165			170			175			
Ala	Thr	Arg	Arg	Asp	His	Val									
					180										

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

Met Ile Lys Ile Ser Asn Leu Ser Lys Ser Phe Ser Gly Gln Thr Val
 1 5 10 15
 Leu Asp His Leu Asn Leu Asp Ile Gln Lys Gly Glu Val Val Ala Leu
 20 25 30
 Ile Gly Ser Ser Gly Ala Gly Lys Ser Thr Phe Leu Arg Ser Leu Asn
 35 40 45
 Tyr Leu Glu Thr Pro Asp Ser Gly Ser Ile Gln Ile Asp Gly Phe Ser
 50 55 60
 Val Asp Phe Ser Lys Ile Thr Gln Glu Glu Ile Leu Ala Leu Arg Arg
 65 70 75 80
 Lys Leu Ser Met Val Phe Gln Gln Phe Asn Leu Phe Glu Arg Arg Thr
 85 90 95
 Ala Leu Asp Asn Val Lys Glu Gly Leu Val Val Lys Lys Leu Ser
 100 105 110
 Asp Gln Glu Ala Thr Lys Ile Ala Lys Glu Leu Ala Lys Val Gly
 115 120 125
 Leu Ser Asp Arg Glu Asn His Tyr Pro Arg His Leu Ser Gly Gln
 130 135 140
 Lys Gln Arg Val Ala Leu Ala Arg Ala Leu Ala Met Lys Pro Asp Val
 145 150 155 160
 Leu Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp Pro Glu Leu Val Gly
 165 170 175
 Glu Val Glu Lys Ser Ile Ala Asp Ala Ala Lys Ser Gly Gln Thr Met
 180 185 190
 Ile Leu Val Ser His Asp Met Pro Phe Val Ala Gln Val Ala Asp Lys
 195 200 205
 Ile Leu Phe Leu Asp Lys Gly Lys Ile Ile Glu Ser Gly Thr Pro Asp
 210 215 220
 Glu Ile Ile His Thr Pro Lys Glu Glu Arg Thr Lys Glu Phe Phe Thr
 225 230 235 240
 Ser Tyr Lys Arg Thr Tyr Ile
 245

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Met Phe Ser Leu Arg Ser Val Phe Asp Gly Ile Pro Arg Ile Val Gln
1 5 10 15
Gln Leu Pro Thr Thr Ile Met Leu Thr Ile Gly Gly Ala Leu Phe Gly
20 25 30
Leu Val Leu Ala Leu Leu Phe Ala Ile Val Lys Ile Asn Arg Val Lys
35 40 45
Ile Leu Tyr Pro Leu Gln Ala Phe Phe Val Ser Phe Leu Lys Gly Thr
50 55 60
Pro Ile Leu Val Gln Leu Met Leu Thr Tyr Tyr Gly Ile Pro Leu Ala
65 70 75 80
Leu Lys Ala Leu Asn Gln Gln Trp Gly Thr Gly Leu Asn Ile Asn Ala
85 90 95
Ile Pro Ala Ala Ala Phe Ala Ile Val Ala Phe Ala Phe Asn Glu Ala
100 105 110
Ala Tyr Ala Ser Glu Thr Ile Arg Ala Ala Ile Leu Ser Val Asn Pro
115 120 125
Gly Glu Ile Glu Ala Ala Arg Ser Leu Gly Met Thr Arg Ala Gln Val
130 135 140
Tyr Arg Arg Val Ile Ile Pro Asn Ala Ala Val Val Ala Thr Pro Thr
145 150 155 160
Leu Ile Asn Ser Leu Ile Gly Leu Thr Lys Gly Thr Ser Leu Ala Phe
165 170 175
Ser Ala Gly Val Val Glu Val Phe Ala Gln Ala Gln Ile Leu Gly Gly
180 185 190
Ala Asp Tyr Arg Tyr Phe Glu Arg Phe Ile Ser Val Ala Leu Val Tyr
195 200 205
Trp Val Val Asn Ile Gly Ile Glu Ser Leu Gly Arg Phe Ile Glu Arg
210 215 220
Lys Met Ala Ile Ser Ala Pro Asp Thr Val Gln Thr Asp Val Lys Gly
225 230 235 240
Asp Leu Arg

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Met	Tyr	Arg	Ile	Asp	Asp	Asp	Glu	Gln	Phe	Val	Leu	Asp	Phe	Leu	Lys
1							5				10			15	
Gln	Glu	Lys	Val	Leu	Leu	Val	His	Gly	Arg	Gly	Phe	Asn	Trp	Gln	Glu
							20				25			30	
Pro	Asp	His	Phe	Arg	Ile	Val	Tyr	Leu	Pro	Arg	Val	Asp	Glu	Leu	Ala
							35				40			45	
Gln	Ile	Gln	Glu	Lys	Met	Thr	Arg	Phe	Leu	Lys	Gln	Tyr	Arg	Arg	
					50					55			60		

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

Met	Asn	Asp	Glu	Ala	Ser	Lys	Gln	Leu	Thr	Asp	Ala	Arg	Phe	Lys	Arg
1							5				10			15	
Leu	Val	Gly	Val	Gln	Arg	Thr	Thr	Phe	Glu	Glu	Ile	Leu	Ala	Val	Leu
							20				25			30	
Lys	Thr	Ala	Tyr	Gln	Leu	Lys	His	Ala	Lys	Gly	Gly	Arg	Lys	Pro	Lys
							35				40			45	
Leu	Ser	Leu	Glu	Asp	Leu	Leu	Met	Ala	Thr	Leu	Gln	Tyr	Val	Arg	Glu
							50				55			60	
Tyr	Arg	Thr	Tyr	Glu	Gln	Ile	Ala	Ala	Asp	Phe	Gly	Ile	His	Glu	Ser
							65				70			75	
Asn	Leu	Ile	Arg	Arg	Ser	Gln	Trp	Val	Glu	Val	Thr	Leu	Val	Gln	Ser
							85				90			95	
Gly	Val	Thr	Ile	Ser	Arg	Thr	Pro	Leu	Ser	Ser	Glu	Asp	Thr	Val	Met
							100				105			110	
Ile	Asp	Ala	Thr	Glu	Val	Gln	Ile	Asn	Arg	Pro	Lys	Lys	Arg	Ile	Ser
							115				120			125	

Glu Ser Phe Trp
130

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

Met Arg Arg Lys Tyr Lys Ser Ile Ala Leu Lys Lys Glu Leu Ala Asn
1 5 10 15
His Ser Gly Lys Lys Lys Phe His Ala Met Lys Ala Gln Ala Ile Val
20 25 30
Thr Ser Gln Gly Arg Ile Val Ser Leu Asp Ile Ala Val Asn Tyr Ser
35 40 45
His Asp Met Lys Leu Phe Lys Met Ser Cys Arg Asn Ile Gly Gln Ala
50 55 60
Gly Lys Ile Leu Ala Asp Ser Gly Tyr Gln Gly Pro Met Lys Ile Tyr
65 70 75 80
Pro Gln Ala Gln Thr Pro Arg Lys Ser Ser Lys Leu Lys Pro Leu Ile
85 90 95
Ala Glu Asp Lys Ala Tyr Asn His Ala Leu Ser Lys Glu Arg Ser Lys
100 105 110
Val Glu Asn Ile Phe Ala Lys Val Lys Thr Phe Lys Met Phe Ser Thr
115 120 125
Thr Tyr Arg Asn His Arg Lys Arg Phe Gly Leu Arg Met Asn Leu Ile
130 135 140
Ala Gly Ile Ile Asn Tyr Glu Leu Gly Phe
145 150

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Met Val Ser Ser Ser Gly Ser Glu Phe Gln Ser Gly Trp Gln Glu His
1 5 10 15
Gln Leu Ile Ala Glu Lys Val Ser Lys Thr Leu Asp Lys Thr Phe Asp
20 25 30
Lys Asp Val Arg Lys Ile Pro Thr Ser Pro Val Leu Ser Lys Ile Cys
35 40 45
Arg

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

Met Ile Lys Ile Leu Ala Ala Cys Gly Ala Gly Val Asn Ser Ser His
1 5 10 15
Gln Ile Lys Ser Ala Leu Glu Glu Glu Leu Ser Asn Arg Gly Tyr Asp
20 25 30
Val His Cys Asp Ala Val Met Val Lys Asp Val Asn Glu Asp Leu Met
35 40 45
Lys Gly Tyr Asp Ile Phe Thr Pro Ile Ala Ala Thr Asp Leu Gly Phe
50 55 60
Glu Pro Gly Ile Pro Val Ile Glu Ala Gly Pro Ile Leu Phe Arg Ile
65 70 75 80
Pro Ala Met Ser Ala Pro Val Phe Asp Asn Ile Arg Leu Pro Ala Lys
85 90 95
Gln Asn Met Val
100

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

Met Asn Thr Lys Met Met Ser Gln Phe Ser Val Met Asp Asn Glu Met
1 5 10 15
Leu Ala Cys Val Glu Gly Gly Asp Ile Asp Trp Gly Arg Glu Ile Ser
20 25 30
Cys Ala Ala Gly Val Ala Tyr Gly Ala Ile Asp Gly Cys Ala Thr Thr
35 40 45
Val

(2) INFORMATION FOR SEQ ID NO:233:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

Met Arg Glu Lys Glu Ile Phe Asp Ser Ile Val Thr Ile Ile Gln Glu
1 5 10 15
Arg Gln Gly Glu Asp Phe Val Val Thr Glu Ser Leu Ser Leu Lys Asp
20 25 30
Asp Leu Asp Ala Asp Ser Val Asp Leu Met Glu Phe Ile Leu Thr Leu
35 40 45
Glu Asp Glu Phe Ser Ile Glu Ile Ser Asp Glu Glu Ile Asp Gln Leu
50 55 60
Gln Ser Val Gly Asp Val Val Lys Ile Ile Gln Gly Lys
65 70 75

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 amino acids

- (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

Met	Ala	His	Gly	Asp	Leu	Leu	Tyr	His	Asp	Gly	Leu	Phe	Phe	Ser	Ala
1				5					10					15	
Lys	Lys	Glu	Asp	Gly	Thr	Tyr	Asp	Phe	His	Glu	Asn	Phe	Glu	Tyr	Val
					20				25				30		
Thr	Pro	Trp	Leu	Lys	Gln	Val	Asp								
					35			40							

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

```

Met Ser Leu Ile Thr His Arg Arg Phe Ile Ser Cys Asn Glu Asn Ile
      1           5           10           15
Lys His Tyr Lys Arg Leu Ile Asp Lys Ala Glu Lys Cys Val Asn Asp
      20          25          30
Leu Met Ala Glu Leu Asn Ser Val Ile Thr Thr Val Thr Gly Ile Glu
      35          40          45
Asn Arg Leu Gly Ala Val Ile Leu Ala Glu Ile Arg Asn Ile His Ala
      50          55          60
Phe Asp Asn Pro Ala Gln Leu Gln Ala Phe Ala Gly Leu Asp Ser Ser
      65          70          75          80
Ile Tyr Gln Ser Gly Gln Ile Asp Leu Val Gly Arg Met Val Lys Arg
      85          90          95
Gly Ser Leu His Leu Arg
      100

```

(2) INFORMATION FOR SEO ID NO: 236:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 117 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

Met Ile Arg Ala Val Phe Phe Ser Ile Asp Asn Asp Met Glu Glu Ala
1 5 10 15
Ala Arg Ser Met Gly Ala Ser Ser Phe Tyr Thr Met Val Arg Val Ile
20 25 30
Ile Pro Tyr Ile Leu Pro Val Val Leu Ser Val Val Val Leu Asn Phe
35 40 45
Asn Ser Leu Leu Ser Asp Tyr Asp Leu Ser Val Phe Leu Tyr His Pro
50 55 60
Leu Phe Gln Pro Leu Gly Ile Val Ile Lys Gln Ser Thr Asp Glu Thr
65 70 75 80
Ala Thr Leu Asn Ala Gln Ala Met Met Phe Val Tyr Ser Val Ile Leu
85 90 95
Met Ile Met Ser Ser Ala Ala Leu Tyr Leu Ser Ser Leu Phe Gln Gly
100 105 110
Lys Arg Gly Lys Arg
115

(2) INFORMATION FOR SEQ ID NO:237:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 101 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

Met Glu Lys Cys Tyr Thr Asp Val Thr Glu Phe Ala Ile Pro Ala Ser
1 5 10 15
Thr Gln Lys Leu Tyr Leu Ser Pro Val Leu Asp Gly Phe Asn Ser Glu
20 25 30

Ile	Ile	Ala	Tyr	Asn	Leu	Ser	Thr	Ser	Pro	Asn	Leu	Glu	Gln	Val	Gln
35							40							45	
Thr	Met	Leu	Glu	Gln	Ala	Phe	Thr	Glu	Lys	His	Tyr	Glu	Asn	Thr	Ile
50							55						60		
Leu	His	Ser	Asp	Gln	Gly	Trp	Gln	Tyr	Gln	His	Asp	Ser	Tyr	His	Arg
65							70					75			80
Phe	Leu	Arg	Val	Arg	Glu	Phe	Lys	His	Leu	Cys	His	Ala	Arg	Glu	Thr
							85					90			95
Ala	Lys	Thr	Thr	Val											
					100										

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

Met	Glu	Ile	Leu	Thr	Thr	Gln	Gln	Val	Arg	Glu	Gly	Tyr	Gln	Ala	Ile
1						5			10					15	
Leu	Ala	Ser	Pro	Leu	Gly	Leu	Gln	Asp	Ala	Phe	Glu	Val	Ala	Gln	Glu
						20				25				30	
Lys	Ser	Gly	Ser	Tyr	Thr	Val	Pro	Pro	Glu	Ile	Asp	Gly	Trp	Lys	Gly
						35			40				45		
Asn	Thr	Glu	Pro	Leu	Arg	Ile	Asp	Tyr	Val	Phe	Thr	Thr	Lys	Glu	Leu
						50			55				60		
Ala	Val	Glu	Asn	Leu	His	Val	Val	Phe	Asp	Gly	Asn	Lys	Ser	Pro	Gln
						65			70			75			80
Val	Ser	Asp	His	Tyr	Gly	Leu	Asn	Ala	Met	Leu	Asn	Trp	Lys		
						85					90				

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

Met Leu Lys His Leu Asn Leu Lys Gly His Leu Leu Thr Ala Ile Ser
1 5 10 15
Tyr Met Ile Pro Ile Val Cys Gly Ala Gly Phe Leu Val Ala Ile Gly
20 25 30
Leu Ala Met Gly Gly Val Pro Asp Ala Leu Val Ala Gly Lys Phe
35 40 45
Thr Ile Trp Asp Ala Leu Ala Thr Met Gly Gly Lys Ala Leu Gly Leu
50 55 60
Leu Pro Val Val Ile Ala Thr Gly Leu Ser Tyr Ser Ile Ala Gly Lys
65 70 75 80
Pro Gly Ile Ala Pro Gly Phe Val Val Gly Leu Ile Ala Asn Ser Val
85 90 95
Gly Ser Gly Phe Ile Gly Gly Ile Leu Gly Gly Tyr Ile Val Gly Phe
100 105 110
Leu Val Gln Ala Ile Ile Lys Lys Val Lys Val Pro Asn Trp Ile Lys
115 120 125
Gly Leu Met Pro Thr Leu Ile Ile Pro Phe Val Pro Leu Trp
130 135 140

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

Met Ile Ala Leu Gly Trp Ser Asn Ile Gly Ala Ala Ile Ala Pro Asp
1 5 10 15
Ala Ala Leu Ala Ser Val Ala Ala Ala Ile Ile Met Val Leu Gly Gly
20 25 30
Asp Phe Thr Lys Thr Gly Ile Gly Val Ala Gln Ala Val Ala Ile Pro
35 40 45
Leu Ala Val Ala Gly Leu Phe Leu Thr Met Ile Val Arg Thr Ile Ser
50 55 60

Val Gly Leu Val His Thr Ala Asp Ala Ala Ala Lys Lys Gly Asp Phe
 65 70 75 80
 Gly Ala Val Glu Arg Ala His Phe Ile Ala Leu Leu Phe Gln Gly Leu
 85 90 95
 Arg Ile Ala Leu Pro Ala Ala Leu Leu Met Val Pro Thr Glu Thr
 100 105 110
 Val Gln Ser Ile Leu Ser Ala Met Pro Asp Trp Leu Lys Asp Gly Met
 115 120 125
 Ala Ile Gly Gly Gly Met Val Val Ala Val Gly Tyr Ala Met Val Ile
 130 135 140
 Asn Met Met Ala Thr Arg Glu Val Trp Pro Phe Phe Ala Leu Gly Phe
 145 150 155 160
 Val Leu Ala Ala Val Ser Asp Ile Thr Leu Ile Gly Phe Gly Ala Ile
 165 170 175
 Gly Val Ala Ile Ala Leu Ile Tyr Leu His Leu Ser Lys Thr Gly Gly
 180 185 190
 Asn Gly Gly Gly Gly Ala Ala Thr Ser Asn Asp Pro Ile Gly Asp Ile
 195 200 205
 Leu Glu Asp Tyr
 210

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Met Leu Asp Val Glu Ala Ile Arg Lys Asp Phe Pro Ile Leu Asp Gln
 1 5 10 15
 Ile Val Asn Asp Glu Pro Leu Val Tyr Leu Asp Asn Ala Ala Thr Thr
 20 25 30
 Gln Lys Pro Leu Val Val Leu Lys Ala Ile Asn Ser Tyr Tyr Glu Gln
 35 40 45
 Asp Asn Ala Asn Val His Arg Gly Val His Thr Leu Ala Glu Arg Ala
 50 55 60
 Thr Ala Ser Leu
 65

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Met	Thr	Lys	Leu	Leu	Asn	Lys	Lys	Trp	Lys	Val	Lys	Ile	Met	Lys	Gln
1															15
Ile	Leu	Leu	Val	Cys	Asn	Ala	Gly	Met	Ser	Thr	Ser	Met	Leu	Val	Lys
															20
															25
															30
Lys	Met	Gln	Gln	Ser	Ala	Thr	Glu	Arg	Gly	Ile	Glu	Ile	Ser	Ile	Gln
															35
															40
Ala	Lys	Ser	Met	Thr	Glu	Ala	Lys	Lys	Asn	Ile	His	Glu	Ala	Asp	Val
															50
															55
Ile	Leu	Ile	Gly	Pro	Gln	Ile	Arg	Tyr	Glu	Leu	Leu	Ala	Val	Lys	Glu
															65
															70
															75
															80
Ile	Ala	Gly	Asn	Ile	Pro	Val	Asp	Thr	Ile	Asp	Met	Arg	Asp	Tyr	Gly
															85
															90
Met	Met	Asn	Gly	Ala	Lys	Val	Leu	Glu	Gln	Ala	Leu	Glu	Trp	Ile	Gly
															100
															105
Glu	Ile	Arg													110
															115

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

Met	Val	Leu	Met	Gln	Iys	Met	His	Gly	Lys	Glu	Leu	Ile	Thr	Leu	Asn
1															15
															5
															10

Gln Thr Val Lys Trp Tyr Lys Val Ser Gly Phe Met Ile Leu Leu Thr
20 25 30
Lys Pro Trp Tyr Tyr Leu Lys Ser Asp Gly Ser Tyr Ala Arg Asn Ala
35 40 45
Trp Gln Gly Asn Tyr Tyr Leu Lys Ser Asp Gly Lys Met Ala Val Asn
50 55 60
Glu Trp Val Tyr Asp Ala Thr Tyr Gln Ala Trp Tyr Tyr Leu Thr Ser
65 70 75 80
Asp Gly Ser Tyr Ala Tyr Ser Thr Trp Gln Gly Asn Tyr Tyr Pro Lys
85 90 95
Ile Gly Trp

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Met Leu Thr Val His Gly Lys Glu Ile Thr Ile Leu Lys Ser Asp Gly
1 5 10 15
Lys Met Ala Val Asn Glu Trp Val Asp Gly Gly Arg Tyr Tyr Val Gly
20 25 30
Ala Asp Gly Val Trp Lys Glu Gly Gln Ala Ser Thr Ala Ser Pro Ser
35 40 45
Asn Asp Ser Asn Ser Glu Tyr Ser Cys Cys Phe Arg Lys Gly Lys Lys
50 55 60
Leu
65

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

Met Asn Asn Asn Phe Asn Asn Phe Asn Asn Met Asp Asp Asp Leu Phe Asn
1 5 10 15
Gln Leu Met Gly Gly Met Arg Gly Tyr Ser Ser Glu Asn Arg Arg Arg Tyr
20 25 30
Leu Ile Asn Gly Arg Glu Val Thr Pro Glu Glu Phe Ala His Tyr Arg
35 40 45
Thr Thr Gly Gln Leu Pro Gly Asn Ala Glu Thr Asp Val Gln Met Pro
50 55 60
Gln Gln Ala Ser Gly Met Lys Gln Asp Gly Val Leu Ala Lys Leu Gly
65 70 75 80
Arg Asn Leu Thr Ala Glu Ala Arg Glu Gly Lys Leu Asp Pro Val Ile
85 90 95
Gly Arg Asn Lys Glu Ile Gln Glu Thr Ser Glu Ile Leu Ser Arg Arg
100 105 110
Thr Lys Asn Asn Pro Val Leu Val Gly Asp Ala Gly Val Gly Lys Thr
115 120 125
Ala Val Val Glu Gly Leu Ala Gln Ala Ile Val Asn Gly Asp Val Pro
130 135 140
Ala Ala Ile Lys Asn Lys Glu Ile Ile Ser Ile Asp Ile Ser Gly Leu
145 150 155 160
Glu Ala Gly Thr Gln Tyr Arg Gly Ser Phe Glu Glu Asn Val Gln Asn
165 170 175
Leu Val Asn Glu Val Lys Glu Ala Gly Asn Ile Ile Leu Phe Phe Asp
180 185 190
Glu Ile His Gln Ile Leu Gly Ala Gly Ser Thr Cys Gly Asp Ser Gly
195 200 205
Ser Lys Gly Leu Ala Asp Ile Leu Ser Gln Ser Ile Ser Leu Val Glu
210 215 220
Asn
225

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

Met Thr Ile Phe Pro Asp Asp Phe Leu Trp Gly Gly Ala Val Ala Ala
 1 5 10 15
 Asn Gln Val Glu Gly Ala Tyr Asn Glu Asp Gly Lys Gly Leu Ser Val
 20 25 30
 Gln Asp Val Leu Pro Lys Gly Gly Leu Gly Glu Ala Thr Glu Asn Pro
 35 40 45
 Thr Glu Asp Asn Leu Lys Leu Ile Gly Ile Asp Phe Tyr His Lys Tyr
 50 55 60
 Lys Glu Asp Ile Ser Leu Phe Ser Glu Met Gly Phe Asn Val Phe Arg
 65 70 75 80
 Thr Ser Ile Ala Trp Ser Arg Ile Phe Pro Lys Gly Asp Glu Glu Glu
 85 90 95
 Pro Asn Glu Ala Gly Leu Lys Tyr Tyr Asp Glu Leu Phe Asp Glu Leu
 100 105 110
 His Ala His Gly Ile Glu Pro Leu Val Thr Leu Ser His Tyr Glu Thr .
 115 120 125
 Pro Leu Tyr Leu Ala Arg Lys Tyr His Gly Trp Ile Asp Arg Lys Asn
 130 135 140
 Asp Ser Phe Leu
 145

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

Met Ile Glu Tyr Lys Asn Val Ala Leu Arg Tyr Thr Glu Lys Asp Val
 1 5 10 15
 Leu Arg Asp Val Asn Leu Gln Ile Glu Asp Gly Glu Phe Met Val Leu
 20 25 30
 Val Gly Pro Ser Gly Ser Gly Lys Thr Thr Met Leu Lys Met Ile Asn
 35 40 45
 Arg Leu Leu Glu Pro Thr Asp Gly Asn Ile Tyr Met Asp Gly Lys Arg
 50 55 60

Ile Lys Asp Tyr Asp Glu Arg Glu Leu Arg Leu Ser Thr Gly Tyr Val
65 70 75 80
Leu Gln Ala Ile Ala Leu Phe Pro Asn Leu Thr Val Ala Glu Asn Ile
85 90 95
Ala Leu Ile Pro Glu Met Lys Gly Trp Ser Lys Glu Glu Ile Thr Lys
100 105 110
Lys Thr Glu Glu Leu Leu Ala Lys Val Gly Leu Pro Val Ala Glu Tyr
115 120 125
Gly His Arg Leu Pro Ser Glu Leu Ser Gly Gly Glu Gln Gln Arg Val
130 135 140
Gly Ile Val Arg Ala Met Ile Gly Gln Pro Lys Ile Phe Leu Met Asp
145 150 155 160
Glu Pro Phe Ser Ala Leu Asp Ala Ile Ser Arg Lys Gln Leu Gln Val
165 170 175
Leu Thr Lys Glu Leu His Lys Glu Phe Gly Met Thr Thr Ile Phe Val
180 185 190
Thr His Asp Thr Asp Glu Ala Leu Lys Leu Ala Asp Arg Ile Ala Val
195 200 205
Leu Gln Asp Gly Glu Ile Arg Gln Val Ala Asn Pro Glu Thr Ile Leu
210 215 220
Lys Val Pro Ala Thr Asp Phe Val Ala Asp Leu Phe Gly Ser Val
225 230 235 240
His Asp

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Met Pro Phe Val Pro Gly Ile Ala Leu Thr Asn Ala Val Arg Asp Ile
1 5 10 15
Met Thr Asn His Ile Asn Ser Gly Met Ser Lys Met Phe Glu Ser Leu
20 25 30
Leu Ile Thr Leu Ala Leu Gly Ala Gly Thr Ser Val Ala Leu Val Leu
35 40 45

Met Asn

50

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

Met Tyr Thr Ile Arg Met Leu Lys Met Gly Ser Glu Ala Ala Ala Lys
1 5 10 15
Ser Ala Gln Glu His Gly Leu Lys Ser Val Glu Val Thr Val Lys Gly
20 25 30
Pro Gly Ser Gly Arg Glu Ser Ala Ile Ser Cys Ala Cys Cys Arg Trp
35 40 45
Ser

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Met Ile Glu Phe Glu Lys Pro Asn Ile Thr Lys Ile Asp Glu Asn Lys
1 5 10 15
Asp Tyr Gly Lys Leu Val Ile Glu Pro Leu Glu Arg Gly Tyr Gly Thr
20 25 30
Ala Leu Gly Asn Ser Leu Arg Arg Val Leu Leu Ala Ser Leu Pro Gly
35 40 45
Ala Ala Val Thr Ser Ile Asn Ile Asp Gly Val Leu His Glu Phe Asp
50 55 60

Thr Val Pro Gly Val Arg Glu Asp Val Met Gln Ile Ile Leu Asn Ile
65 70 75 80
Lys Gly Ile Ala Val Lys Ser Tyr Val Glu Asp Glu Lys Ile Ile Glu
85 90 95
Leu Asp Val Glu Gly Pro Ala Glu Val Thr Ala Gly Asp Ile Leu Thr
100 105 110
Asp Ser Asp Ile Glu Ile Val Asn Pro Asp His Tyr Leu Phe Thr Ile
115 120 125
Gly Glu Gly Ser Ser Leu Lys Ala Thr Met Thr Val Asn Ser Gly Arg
130 135 140
Gly Tyr Val Pro Ala Asp Glu Asn Lys Lys Asp Asn Ala Pro Val Gly
145 150 155 160
Thr Leu Ala Val Asp Ser Ile Tyr Thr Pro Val Thr Lys Val Asn Tyr
165 170 175
Gln Val Glu Pro Ala Arg Val Gly Ser Asn Asp Gly Phe Asp Lys Leu
180 185 190
Thr Leu Glu Ile Leu Thr Asn Gly Thr Ile Ile Pro Glu Asp Ala Leu
195 200 205
Gly Leu Ser Ala Arg Ile Leu Thr Glu His Leu Asp Leu Phe Thr Asn
210 215 220
Leu Thr Glu Ile Ala Lys Ser Thr Glu Val Met Lys Glu Ala Asp Thr
225 230 235 240
Glu Ser Asp Asp Arg Ile Leu Asp Arg Thr Ile Glu Glu Leu Asp Leu
245 250 255
Ser Val Arg Ser Tyr Asn Cys Leu Lys Arg Ala Gly Ile Asn Thr Val
260 265 270
His Asp Leu Thr Glu Lys Ser Glu Ala Glu Met Met Lys Val Arg Asn
275 280 285
Leu Gly Arg Lys Ser Leu Glu Glu Val Lys Leu Lys Leu Ile Asp Leu
290 295 300
Gly Leu Gly Leu Lys Asp Lys
305 310

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

Met Asp Ile Glu Lys Gln Arg Gly Ile Ser Val Thr Ser Ser Val Met
 1 5 10 15
 Gln Phe Asp Tyr Asp Gly Lys Arg Val Asn Ile Leu Asp Thr Pro Gly
 20 25 30
 His Glu Asp Phe Ser Glu Asp Thr Tyr Arg Thr Leu Met Ala Val Asp
 35 40 45
 Ala Ala Val Met Val Val Asp Ser Ala Lys Gly Ile Glu Ala Gln Thr
 50 55 60
 Lys Lys Leu Phe Glu Val Val Lys His Arg Gly Ile Pro Val Phe Thr
 65 70 75 80
 Phe Met Asn Lys Leu Asp Arg Asp Gly Arg Glu Pro Leu Asp Leu Leu
 85 90 95
 Gln Glu Leu Glu Glu Ile Leu Gly Ile Ala Ser Tyr Pro Met Asn Trp
 100 105 110
 Pro Ile Gly Met Gly Lys Ala Phe Glu Gly Leu Tyr Asp Leu Tyr Asn
 115 120 125
 Gln Arg Leu Glu Leu Tyr Lys Gly Asp Glu Arg Phe Ala Ser Pro Arg
 130 135 140
 Arg Trp Arg Gln Thr Phe Trp
 145 150

(2) INFORMATION FOR SEQ ID NO:252:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Met Ala Val Ile Ala Glu Arg Lys Ala Tyr Tyr His Asp Pro Val Glu
 1 5 10 15
 Asp Ala Ile Ile Met Lys Arg Glu Ile Asp Glu Gly
 20 25

(2) INFORMATION FOR SEQ ID NO:253:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

Met Asn Glu Thr Trp Ser Arg Thr Ala Leu Thr Leu Leu Lys His Gly
1 5 10 15
Ser Glu Val Asn Leu Glu Arg Ala Leu Ser Val Asn Gly Arg Leu Gly
20 25 30
Gly His Val Val Thr Gly His Ile Asp Gly Thr Gly Lys Ile Ser Ser
35 40 45
Ile Lys Lys Asp Asp Asn Ala Val Trp Tyr Gln Ile Asn Thr Gln Lys
50 55 60
Glu Ile Leu Asp Leu Ile Val Glu Lys Gly Ser Ile Thr Ile Asp Gly
65 70 75 80
Ile Ser Leu Thr Val Ala Lys Val Ser Lys Val Asn Phe Ser Val Ser
85 90 95
Val Ile Pro His Thr Leu Lys Gln Thr Ile Leu Lys Ser Lys Gln Val
100 105 110
Gly Ser Thr Val Asn Leu Glu Asn Asp Ile Leu Gly Lys Tyr Val Gln
115 120 125
Lys Leu Met Asp Asn Ser Pro Lys Ser Glu Ile Ser Lys Glu Leu Leu
130 135 140
Tyr Gln Asn Gly Phe
145

(2) INFORMATION FOR SEQ ID NO:254:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

Met Asn Trp Ser Ala Leu Glu Gln Gln Ile Val Asp Glu Leu Lys Ile
1 5 10 15
Tyr Ile Ala Pro Lys Ile Phe Gly Gly Ser Ala Lys Phe Pro Val Gly
20 25 30

Gly Glu Gly Ile Ser Leu Pro Asn Asp Ala Ile Arg Leu Lys Pro Tyr
 35 40 45
 Ala Phe Ser Gln Xaa Gly Xaa Asp Tyr Leu Ile Glu Ser Glu Val Ile
 50 55 60
 Tyr Pro Cys Ser Gln Glu
 65 70

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

Met Val Leu Phe Leu Val Pro Gln Leu Arg Asn Ala Tyr Gly Thr Ala
 1 5 10 15
 Ala Ile Gly Ile Ile Cys Gly Leu Tyr Trp Ala Val Ser Ser Asn Met
 20 25 30
 Thr Val Glu Ala Thr Gln Arg Leu Thr Gly Gly Gly Phe Ala Ile
 35 40 45
 Gly His Gln Gln Gln Phe Ala Ile Trp Phe Val Asp Lys Val Ala Gly
 50 55 60
 Arg Phe Gly Lys Lys Glu Glu Ser Leu Asp Asn Leu Lys Leu Pro Lys
 65 70 75 80
 Phe Leu Ser Ile Phe His Asp Thr Val Val Ala Ser Ala Thr Phe Asp
 85 90 95
 Ala Arg Ile Leu Arg Gly His Ser Phe Asn Leu Gly Ser Arg His Tyr
 100 105 110
 Val

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

Met Leu Ile Asn Ser Leu Asn Gln Ser Tyr Ile Ser Ala Lys Arg Ile
1 5 10 15
Glu Glu Val Phe Ala Glu Ser Pro Glu Asn Ile His Ser Glu Leu Glu
20 25 30
Gln Lys Gln Val Thr Ser Gly Arg Val Leu Gln Val Gln Glu Leu Thr
35 40 45
Phe Thr Tyr Pro Asp Ala Ala Gln Pro Ser Leu Arg Asp Ile Ser Phe
50 55 60
Asp Met Thr Gln Gly Gln Ile Leu Gly Ile Ile Gly Gly Thr Gly Ser
65 70 75 80
Gly Lys Ser Ser Leu Val Gln Leu Leu Gly Leu Tyr Pro Val Asp
85 90 95
Lys Gly Asn Ile Asp Leu Tyr Gln Asn Gly Arg Ser Pro Leu Asn Leu
100 105 110
Glu Gln Trp Arg Ser Trp Ile Ala Tyr Val Pro Gln Lys Val Lys Leu
115 120 125
Phe Lys Gly Thr Ile Arg Ser Asn Leu Thr Leu Gly Leu Asn Gln Glu
130 135 140
Val Ser Asp Gln Lys Leu Trp Gln Ala Leu Glu Ile Ala Gln Ala Lys
145 150 155 160
Asp Phe Val Ser Glu Lys Glu Gly Leu Leu Asp Ala Leu Ile Glu Ala
165 170 175
Gly Gly Arg Asn Phe Ser Gly Gly Gln Lys Gln Arg Leu Ser Ile Ala
180 185 190
Arg Ala Val Leu Arg Gln Ala Pro Phe Ile Ile Leu Asp Asp Ala Thr
195 200 205
Ser Ala Leu Asp Thr Ile Thr Glu Ser Lys Leu Leu Lys Ala Ile Arg
210 215 220
Glu Asn Phe Pro Asn Thr Ser Leu Ile Leu Ile Ser Gln Arg Thr Ser
225 230 235 240
Thr Leu Gln Met Ala Asp Gln Ile Leu Leu Leu Glu Lys Gly Glu Leu
245 250 255
Leu Ala Val Gly Lys His Asp Asp Leu Met Lys Ser Ser Gln Val Tyr
260 265 270
Arg Glu Ile Asn Ala Ser Gln His Gly Lys Glu Asp
275 280

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

```

Met Lys Asp Pro Glu Ser Arg Leu Tyr Ile Leu Leu Lys Asp Gly Gln
1           5           10           15
Val Ile Gly Thr Cys Thr Val Asp Leu Ser Thr Asn Thr Asn Tyr Phe
20          25          30
Tyr Gly Leu Ala Ile Leu Glu Pro Glu Arg Gly Lys Gly Tyr Gly Ser
35          40          45
Tyr Leu Ala Lys Ser Leu Val Asn Gln Leu Ile Glu Gln Asn Asp Lys
50          55          60
Glu Phe Gln Ile Ala Val Glu Asp Ser Asn Val Gly Ala Lys Arg Leu
65          70          75          80
Tyr Glu Lys Ile Gly Phe Val Lys Gln Thr Gln Val Val Tyr Leu Asn
85          90          95
Glu Lys Gly Ala Arg Asp Ser Glu Val
100         105

```

(2) INFORMATION FOR SEQ ID NO:258:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

```

Met Phe Ala Leu Ser Ser Asn Lys Glu Leu Ala Glu Arg Val Ala Gln
1           5           10           15
Glu Ile Gly Ile Glu Leu Gly Lys Ser Ser Val Arg Gln Phe Ser Asp
20          25          30
Gly Glu Ile Gln Val Asn Ile Glu Glu Ser Ile Arg Gly Lys His Val
35          40          45
Phe Ile Leu Gln Ser Thr Ser Ser Pro Val Asn Asp Asn Leu Leu Glu
50          55          60

```

Ile Leu Ile Met Val Asp Ala Leu Lys Arg Ala Ser Ala Glu Ser Val
65 70 75 80
Asn Val Val Met Pro Tyr Tyr Gly Tyr Ala Arg Gln Asp Arg Lys Ala
85 90 95
Arg Ala Arg Glu Pro Ile Thr Ser Lys Leu Val Ala Asn Met Leu Glu
100 105 110
Val Ala Gly Val Asp Arg Leu Leu Thr Ile Asp Leu His Ala Ala Gln
115 120 125
Ile Gln Gly Phe Phe Asp Ile Pro Val Asp His Leu Met Gly Ala Pro
130 135 140
Leu Ile Ala Asp Tyr Phe Glu Arg Pro Gly Met Val Gly Ser Asp Tyr
145 150 155 160
Val Val Val Ser Pro Asp His Gly Gly Val Thr Arg Ala Arg Lys Leu
165 170 175
Ala Glu Phe Leu Lys Thr Ser Ile Ala Ile Ile Glu Lys Arg Arg Ser
180 185 190
Val Asp Lys Met Asn Thr Ser Glu Val Met Asn Thr Ile Gly Lys Val
195 200 205
Glu Gly Asn His Leu
210

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

Met Ile Ser Phe Leu Leu Leu Val Leu Val Trp Gly Phe Tyr Ile
1 5 10 15
Gly Tyr Arg Arg Gly Leu Leu Leu Gln Val Tyr Tyr Leu Ile Ser Ala
20 25 30
Met Ala Ser Ala Phe Met Ala Gly Gln Phe Tyr Lys Gly Leu Gly Glu
35 40 45
Gln Phe His Leu Leu Leu Pro Tyr Ala Asn Ser Gln Glu Gly Gln Gly
50 55 60
Thr Phe Phe Phe Pro Ser Asp Gln Leu Phe Gln Leu Asp Lys Val Phe
65 70 75 80

Tyr Ala Gly Ile Gly Tyr Leu Leu Val Phe Gly Ile Val Tyr Ser Ile
85 90 95
Gly Arg Leu Leu Gly Leu Leu Leu His Leu Ile Pro Ser Lys Lys Leu
100 105 110
Gly Gly Lys Leu Phe Gln Val Ser Ala Gly Ile Leu Ser Met Leu Val
115 120 125
Thr Leu Phe Val Leu Gln Met Ala Leu Thr Ile Leu Ala Thr Ile Pro
130 135 140
Met Ala Val Ile Gln Asn Pro Leu Glu Lys Ser Ile Val Ala Lys His
145 150 155 160
Ile Ile Gln Ser Ile Pro Ile Thr Thr Ser Trp Leu Lys Gln Ile Trp
165 170 175
Val Thr Asn Leu Ile Gly
180

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

Met Arg Ala Phe Ser Asp Phe Gly Thr Pro Met Leu Ile Gly Glu Gly
1 5 10 15
Tyr Arg Thr Phe Pro Val Leu Ile Tyr Thr Gln Phe Ile Ser Glu Val
20 25 30
Gly Gly Asn Ser Ala Phe Ala Ile Met Ala Ile Ile Ile Ala Leu Ala
35 40 45
Ile Phe Leu Ile Gln Lys His Ile Ala Asn Arg Tyr Ser Phe Ser Met
50 55 60
Asn Leu Leu His Pro Ile Glu Pro Lys Lys Thr Thr Lys Gly Lys Met
65 70 75 80
Ala Ala Ile Tyr Ala Thr Val Tyr Gly Ile Ile Phe Ile Ser Val Leu
85 90 95
Pro Gln Ile Tyr Leu Ile Tyr Thr Ser Phe Leu Lys Thr Ser Gly Met
100 105 110
Val Phe Val Lys Gly Tyr Ser Pro Asn Ser Tyr Lys Val Ala Phe Asn
115 120 125

Arg Met Gly Ser Ala Ile Phe Asn Thr Ile Arg Ile Pro Leu Ile Ala
130 135 140
Leu Val Leu Val Val Pro Ile Tyr Asp Ile Tyr Leu Leu Pro Ser Arg
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Met Val Pro Tyr Ile Val Pro Gly Thr Val Leu Gly Ile Ala Phe Ile
1 5 10 15
Ser Ser Phe Asn Thr Gly Leu Phe Gly Ser Gly Phe Leu Met Ile Thr
20 25 30
Gly Thr Ala Phe Ile Leu Ile Met Ser Leu Ser Val Arg Arg Leu Pro
35 40 45
Tyr Thr Ile Arg Ser Ser Val Ala Ser Leu Gln Gln Ile Ala Pro Ser
50 55 60
Ile Glu Glu Ala Ala Gly Lys Leu Arg Lys
65 70

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

Met Ile Phe Ile Pro Met Ala Ala Tyr Ser Ile Ala Arg Asn Met Ser
1 5 10 15
Lys Arg Lys Ala Phe Thr Ile His Val Tyr Pro Leu Asn Pro Arg Asn
20 25 30

Leu Arg Thr Phe Pro Ser His His Asp Ser Asp Tyr Gly Tyr Asp Glu
35 40 45

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

Met Lys Phe Arg Lys Leu Ala Cys Thr Val Leu Ala Gly Ala Ala Val
1 5 10 15
Leu Gly Leu Ala Ala Cys Gly Asn Ser Gly Gly Ser Lys Asp Ala Ala
20 25 30
Lys Ser Gly Gly Asp Gly Ala Lys Thr Glu Ile Thr Trp Trp Ala Phe
35 40 45
Pro Val Phe Thr Gln Glu Lys Thr Gly Asp Gly Val Gly Thr Tyr Glu
50 55 60
Lys Ser Ile Ile Gln Ala Phe
65 70

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

Met Asn Ser Gln Gln Lys Pro Gln Glu Ile Lys Val Glu Glu Pro Val
1 5 10 15
Glu Ser Lys Glu Glu Thr Val Asn Gln Pro Val Glu Gln Pro Lys Val
20 25 30
Glu Thr Pro Ala Val Glu Lys Gln Thr Glu Pro Thr Glu Glu Pro Lys
35 40 45

Val Glu Val Thr Ser Ile Pro Gln Thr Thr Arg Tyr Glu Glu Asp Leu
50 55 60
Thr Lys Glu His Gly Thr Arg Glu Val Val Lys Glu Gly Lys Asn Gly
65 70 75 80
Ser Arg Thr Val Thr Thr Pro Tyr Ile Leu Asn Ala Thr Asp Gly Thr
85 90 95
Thr Thr Glu Gly Thr Ser Thr Thr Asp Glu Ala Glu Met Glu Lys Glu
100 105 110
Val Val Arg Val Gly Thr Lys Pro Lys Glu Lys Leu Ala Pro Val Leu
115 120 125
Ser Leu Thr Ser Val Thr Asp Asn Ala Met Leu Arg Ser Ala Arg Leu
130 135 140
Thr Tyr His Leu Glu Asn Thr Asp Ser Val Asp Val Lys Lys Ile His
145 150 155 160
Ala Glu Ile Lys Asn Gly Asp Lys Val Val Lys Thr Ile Asp Leu Ser
165 170 175
Lys Glu Arg Leu Ser Asp Ala Val Asp Gly Leu Glu Leu Tyr Lys Asp
180 185 190
Tyr Lys Ile Val Thr Ser Met Thr Tyr Asp Arg Gly Asn Gly Glu Glu
195 200 205
Thr Ser Thr Leu Glu Glu Thr Pro Leu Arg Leu Asp Leu Lys Lys Val
210 215 220
Glu Leu Lys Asn Ile Gly Ser Thr Asn Leu Val Lys Val Asn Glu Asp
225 230 235 240
Gly Thr Glu Val Ala Ser Asp Phe Leu Thr Ser Lys Pro Val Asp Val
245 250 255
Gln Asn Tyr Tyr Leu Lys Val Thr Ser Arg Asp Asn Lys Val Val Ser
260 265 270
Pro Pro Ser
275

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

Met Ala Val Met Lys Ile Glu Tyr Tyr Ser Gln Val Leu Asp Met Glu
 1 5 10 15
 Trp Gly Val Asn Val Leu Tyr Pro Asp Ala Asn Arg Val Glu Glu Pro
 20 25 30
 Glu Cys Glu Asp Ile Pro Val Leu Tyr Leu Leu His Gly Met Ser Gly
 35 40 45
 Asn His Asn Ser Trp Leu Lys Arg Thr Asn Val Glu Arg Leu Leu Arg
 50 55 60
 Gly Thr Asn Leu Ile Val Val Met Pro Asn Thr Ser Asn Gly Trp Tyr
 65 70 75 80
 Thr Asp Thr Gln Tyr Gly Phe Asp Tyr Tyr Thr Ala Leu Ala Glu Glu
 85 90 95
 Leu Pro Gln Val Pro Glu Thr Leu Leu Pro
 100 105

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

Met Arg Leu Leu Ala Met Lys Met Lys Gln Ile Ser Asp Thr Thr Leu
 1 5 10 15
 Lys Ile Thr Met Ser Leu Glu Asp Leu Met Asp Arg Gly Met Glu Ile
 20 25 30
 Ala Asp Phe Leu Val Pro Gln Glu Lys Thr Glu Glu Phe Phe Tyr Ala
 35 40 45
 Ile Leu Gly
 50

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

Met Leu Pro Ile Ile Cys Cys Gly Glu Ser Leu Glu Thr Tyr Glu Ala
1 5 10 15
Gly Lys Ala Ala Glu Phe Val Gly Ala Gln Val Ser Ala Ala Leu Ala
20 25 30
Gly Leu Thr Ala Glu Gln Val Ala Ala Ser Val Ile Ala Tyr Glu Pro
35 40 45
Ile Trp Ala Ile Gly Thr Gly Lys Ser Ala Ser Gln Asp Asp Ala Gln
50 55 60
Lys Met Cys Lys Val Val Arg Asp Val Val Ala Ala Asp Phe Gly Gln
65 70 75 80
Glu Val Ala Asp Lys Val Arg Val Gln Tyr Gly Gly Ser Val Lys Pro
85 90 95
Glu Asn Val Ala Ser Tyr Met Ala Cys Pro Asp Val Asp Gly Ala Leu
100 105 110
Val Gly Gly Ala Ser Leu Glu Ala Glu Ser Phe Leu Ala Leu Leu Asp
115 120 125
Phe Val Lys
130

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

Met Phe Val Glu Ala Cys Lys Ala Val Val Arg Ala Asn Glu Glu Tyr
1 5 10 15
Val Pro Pro Tyr Gly Ile Gly Gly Thr Leu Tyr Leu Arg Pro Leu Leu
20 25 30
Ile Gly Val Gly Asp Ile Ile Gly Val Lys Pro Ala Glu Glu Tyr Ile
35 40 45
Phe Thr Ile Phe Ala Met Pro Val Gly Asn Tyr Phe Lys Gly Gly Leu
50 55 60

Val	Pro	Thr	Asn	Phe	Leu	Ile	Gln	Asp	Glu	Tyr	Asp	Arg	Ala	Ala	Pro
65															80
Asn	Gly	Thr	Gly	Ala	Ala	Lys	Val	Gly	Gly	Asn	Tyr	Ala	Ala	Ser	Leu
						85			90						95
Leu	Pro	Gly	Lys	Met	Ala	Lys	Ser	Arg	His	Phe	Ser	Asp	Val	Ile	Tyr
						100			105						110
Leu	Asp	Pro	Ser	Thr	His	Thr	Lys	Ile	Glu	Glu	Val	Gly	Ser	Ala	Asn
						115			120						125
Phe	Phe	Gly	Ile	Thr	Ala	Asp	Asn	Glu	Phe	Val	Thr	Pro	Leu	Ser	Pro
						130			135						140
Ser	Ile	Leu	Pro	Ser	Ile	Thr	Lys	Tyr	Ser	Leu	Leu	Tyr	Leu	Ala	Glu
145							150			155					160
His	Arg	Leu	Gly	Leu	Thr	Pro	Ile	Glu	Gly	Asp	Val	Pro	Ile	Asp	Asn
							165			170					175
Leu	Asp	Arg	Phe	Val	Lys	Ala	Gly	Ala	Cys	Gly	Thr	Ala	Ala	Val	Ile
						180			185						190
Ser	Pro	Ile	Gly	Gly	Ile	Gln	His	Gly	Asp	Asp	Phe	His	Val	Ile	Leu
						195			200						205

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

Met	Val	Met	Ile	Ser	Met	Leu	Phe	Tyr	Ser	Glu	Thr	Glu	Val	Gly	Pro
1							5			10					15
Val	Thr	Arg	Lys	Leu	Tyr	Asn	Glu	Leu	Thr	Gly	Ile	Gln	Phe	Gly	Asp
							20			25					30
Ile	Glu	Ala	Pro	Glu	Gly	Trp	Ile	Val	Lys	Val	Asp				
							35			40					

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

Met	Thr	Ala	Ser	Pro	Leu	Lys	Lys	Ser	Ile	Lys	Lys	Lys	Asn	Arg	Lys
1					5				10				15		
Leu	Thr	Asn	Lys	Xaa	Glu	Lys	His	Met	Ser	Lys	Ile	Ile	Gly	Ile	Asp
					20				25				30		
Leu	Gly	Thr	Thr	Asn	Ser	Ala	Val	Ala	Val	Leu	Glu	Gly	Thr	Glu	Ser
	35								40				45		
Lys	Ile	Ile	Ala	Asn	Pro	Glu	Gly	Asn	Arg	Thr	Thr	Pro	Ser	Val	Val
	50					55				60					
Ser	Phe	Lys	Asn	Gly	Glu	Ile	Ile	Val	Gly	Asp	Ala	Ala	Lys	Arg	Gln
	65				70				75				80		
Ala	Val	Thr	Asn	Pro	Asp	Thr	Val	Ile	Ser	Ile	Lys	Ser	Lys	Met	Gly
		85							90				95		
Thr	Ser	Glu	Lys	Val	Ser	Ala	Asn	Gly	Lys	Glu	Tyr	Thr	Pro	Gln	Glu
	100							105				110			
Ile	Ser	Ala	Met	Ile	Leu	Gln	Tyr	Leu	Lys	Gly	Tyr	Ala	Glu	Asp	Tyr
	115						120					125			
Leu	Gly	Glu	Lys	Val	Thr	Lys	Ala	Val	Ile	Thr	Val	Pro	Ala	Tyr	Phe
	130					135				140					
Asn	Asp	Ala	Gln	Arg	Gln	Ala	Thr	Lys	Asp	Ala	Gly	Lys	Ile	Ala	Gly
	145						150			155			160		
Leu	Glu	Val	Xaa	Arg	Ile	Val	Asn	Glu	Pro	Thr	Ala	Ala	Leu	Ala	
		165					170					175			
Tyr	Gly	Leu	Asp	Lys	Thr	Asp	Lys	Glu	Glu	Lys	Ile	Leu	Val	Phe	Asp
	180					185				190					
Leu	Gly	Gly	Gly	Thr	Phe	Asp	Val	Ser	Ile	Leu	Glu	Leu	Gly	Asp	Gly
	195						200				205				
Val	Phe	Asp	Val	Leu	Ser	Thr	Ala	Gly	Asp	Asn	Lys	Leu	Gly	Gly	Asp
	210					215				220					
Asp	Phe	Asp	Gln	Lys	Ile	Ile	Asp	His	Leu	Val	Ala	Glu	Phe	Lys	Lys
	225						230			235			240		
Glu	Asn	Gly	Ile	Arg	Leu	Val	Tyr								
					245										

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

Met Lys Leu Ile Val Asp Leu Ile Tyr Glu Gly Gly Phe Lys Lys Met
1 5 10 15
Arg Gln Ser Ile Ser Asn Thr Ala Glu Tyr Gly Asp Tyr Val Ser Gly
20 25 30
Pro Arg Val Ile Thr Glu Gln Val Lys Glu Asn Met Lys Ala Val Leu
35 40 45
Ala Asp Ile Gln Asn Gly Lys Phe Ala Asn Asp Phe Val Asn Asp Tyr
50 55 60
Lys Ala Gly Arg Pro Lys Leu Thr Ala Tyr Arg Glu Gln Ala Ala Asn
65 70 75 80
Leu Glu Ile Glu Lys Val Gly Ala Glu Leu Arg Lys Ala Met Pro Phe
85 90 95
Val Gly Lys Asn Asp Asp Ala Phe Lys Ile Tyr Asn
100 105

(2) INFORMATION FOR SEQ ID NO:272:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

Met Leu Leu Ser Ala Phe His Lys Tyr Glu Asn Gln Leu Asp Lys Val
1 5 10 15
Arg Phe Ile Gly Leu His Thr Gly His Leu Gly Phe Tyr Thr Asp Tyr
20 25 30
Arg Asp Phe Glu Leu Asp Lys Leu Val Thr Asn Leu Gln Leu Asp Thr
35 40 45
Gly Ala Arg Val Ser Tyr Pro Val Leu Asn Val Lys Val Phe Leu Glu
50 55 60
Asn Gly Glu Val Lys Ile Phe Arg Ala Leu Asn Glu Ala Ser Ile Arg
65 70 75 80

Arg Ser Asp Arg Thr Met Val Ala Asp Ile Val Ile Asn Gly Val Pro
85 90 95
Phe Glu Arg Phe Arg Gly Asp Gly Leu Thr Val Ser Thr Pro Thr Gly
100 105 110
Ser Thr Ala Tyr Asn
115

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

Met Gly Ala Gln Leu Ala Arg Glu Phe Lys His Glu Ala Asp Ile Val
1 5 10 15
Val Gly Val Pro Asn Ser Ser Leu Ser Ala Ala Met Gly Phe Ala Glu
20 25 30
Glu Ser Gly Leu Pro Asn Glu Met Gly Leu Ile Lys Asn Gln Tyr Thr
35 40 45
Gln Arg Thr Phe Ile Gln Pro Thr Gln Glu Leu Arg Glu Gln Gly Val
50 55 60
Arg Met Lys Leu Ser Ala Val Ser Gly Val Val Lys Gly Lys Arg Val
65 70 75 80
Val Met Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Arg Arg Ile
85 90 95
Val Gln Leu Leu Lys Glu Ala Gly Ala Thr Glu Val His Val Ala Ile
100 105 110
Gly Ser Pro Ala Leu Ala Tyr Pro Cys Phe Tyr Gly Ile Asp Ile Gln
115 120 125
Thr Arg Gln Glu Leu Ile Ala Ala Asn His Thr Val Glu Glu Thr Arg
130 135 140
Gln Ile Ile Gly Ala Asp Ser Leu Thr Tyr Leu Ser Ile Asp Ser Leu
145 150 155 160
Ile Glu Ser Ile Gly Ile Glu Thr Asp Ala Pro Asn Gly Gly Leu Cys
165 170 175
Val Ala Tyr Phe Asp Gly Asp Tyr Pro Thr Pro Leu Tyr Asp Tyr Glu
180 185 190

Glu Asp Tyr Arg Arg Ser Leu Glu Glu Lys Thr Ser Phe Tyr Lys
195 200 205

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Met Lys Ile Leu Val Thr Gly Phe Asn Pro Phe Gly Gly Glu Lys Ile
1 5 10 15
Asn Pro Ala Leu Glu Ala Val Lys Leu Leu Pro Ser Glu Ile Asn Gly
20 25 30
Ala Glu Val Arg Trp Val Glu Ile Pro Thr Val Phe Tyr Lys Ser Ser
35 40 45
Glu Val Leu Glu Ala Glu Ile Leu Arg Tyr Gln Pro Asp Ala Val Leu
50 55 60
Cys Ile Gly Gln Ala Gly Gly Arg Thr Gly Leu Thr Pro Glu Arg Val
65 70 75 80
Ala Ile Asn Gln Asp Asp Ala Arg Ile Pro Asp Asn Glu Gly Asn Gln
85 90 95
Pro Ile Asp Thr Pro Ile Arg Ile Asp Gly Ala Ser Ala Tyr Phe Ser
100 105 110
Ser Leu Pro Ile Lys Ala Met Val Gln Ala Asn Lys Lys Glu Gly Leu
115 120 125
Thr Gly Ser Leu Phe Pro Ile Arg Ala Gly Thr Phe Val Cys Ser His
130 135 140
Leu Met Tyr Gln Ala Leu Tyr Leu Val Glu Lys Lys Phe Pro Tyr Val
145 150 155 160
Lys Ala Gly Phe Met His Ile Pro Tyr Met Met Glu Gln Val Val Asn
165 170 175
Arg Pro Thr Thr Pro Thr Met Ser Leu Val Asp Ile Arg Arg Gly Ile
180 185 190
Glu Ala Ala Ile Gly Ala Met Ile Glu His Gly Asp Gln Glu Leu Thr
195 200 205
Leu Val Gly Gly Glu Ile His
210 215

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

Met Leu Val Pro Lys Arg Val Lys His Arg Arg Glu Phe Arg Gly Lys
1 5 10 15
Met Arg Gly Glu Ala Lys Gly Gly Lys Glu Val Ala Phe Gly Glu Tyr
20 25 30
Gly Leu Gln Ala Thr Thr Ser His Trp Ile Thr Asn Arg Gln Ile Glu
35 40 45
Ala Ala Arg Ile Ala Met Thr Arg Tyr Met Lys Arg Gly Gly Lys Val
50 55 60
Trp Ile Lys Ile Phe Pro His Lys Ser Tyr Thr Ala Lys Ala Ile Gly
65 70 75 80
Val Arg Met Gly Ser Gly Lys Gly Ala Pro Glu Gly Trp Val Ala Pro
85 90 95
Val Lys Arg Gly Lys Val Met Phe Glu Ile Ala Gly Val Ser Glu Glu
100 105 110
Ile Ala Arg Glu Ala Leu Arg Leu Ala Ser His Lys Leu Pro Val
115 120 125

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

Met Gly Trp Trp Arg Glu Thr Ile Asp Ile Val Lys Glu Asn Asp Pro
1 5 10 15

Ala Ala Arg Thr Thr Leu Glu Val Leu Leu Thr Tyr Pro Gly Val Lys
 20 25 30
 Ala Leu Ala Ala His Arg Leu Ser His Phe Leu Trp Lys Tyr Asp Phe
 35 40 45
 Lys Leu Leu Ala Arg Met His Ser Gln Phe Trp Arg Phe Trp Thr Gln
 50 55 60
 Ile Glu Ile His Pro Gly Ala Gln Ile Asp Ser Gly Val Phe Ile Asp
 65 70 75 80
 His Gly Ser Gly Leu Val Ile Gly Glu Thr Ala Ile Val Glu Lys Gly
 85 90 95
 Val Leu Leu Tyr His Gly Val Thr Leu Gly Gly Thr Gly Lys Asp Cys
 100 105 110
 Gly Lys Arg His Pro Thr Val Arg Lys Gly Ala Leu Ile Ser Ala His
 115 120 125
 Ala Gln Val Ile Gly Pro Val Glu Ile Gly Glu Asn Ala Lys Val Gly
 130 135 140
 Ala Ala Ala Val Val Val Ala Asp Val Pro Ser Asp Val Thr Val Val
 145 150 155 160
 Gly Ile Pro Ala Lys Ile Val Arg Leu His Gly Lys Lys Asp Glu Pro
 165 170 175
 Val Ile His Glu Val Glu Glu Lys Arg Glu Tyr Tyr Val Asn Lys Leu
 180 185 190
 Glu Gln Ala Lys Asp Ala Ser His Arg Ser Ser Gly Leu
 195 200 205

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

Met Leu Phe Tyr Leu Leu Arg Asp Gly Lys Gly Leu Arg Asn Tyr Leu
 1 5 10 15
 Thr Gln Phe Ile Pro Ser Lys Leu Lys Glu Pro Val Gly Gln Val Leu
 20 25 30
 Ser Asp Val Asn Gln Gln Leu Ser Asn Tyr Val Arg Gly Gln Val Thr
 35 40 45

Val Ala Ile Ile Val Ala Val Met Phe Ile Ile Phe Phe Lys Ile Ile
50 55 60
Gly Leu Arg Tyr Ala Val Thr Leu Gly Val Thr Ala Gly Ile Leu Asn
65 70 75 80
Leu Val Pro Tyr Leu Gly Ser Phe Leu Ala Met Leu Pro Ala Leu Val
85 90 95
Leu Gly Leu Ile Ala Gly Pro Val Met Leu Leu Lys Val Val Ile Val
100 105 110
Phe Ile Val Glu Gln Thr Ile Glu Gly Arg Phe Val Ser Pro Leu Ile
115 120 125
Leu Gly Ser Gln Leu Asn Ile His Pro Ile Asn Val Leu Phe Val Leu
130 135 140
Leu Thr Ser Gly Ser Met Phe Gly Ile Trp Gly Val Leu Leu Gly Ile
145 150 155 160
Pro Val Tyr Ala Ser Ala Lys Val Val Ile Ser Ala Ile Phe Glu Trp
165 170 175
Tyr Lys Val Val Ser Gly Leu Tyr Glu Leu Glu Gly Glu Val Lys
180 185 190
Ser Glu Gln
195

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

Met Thr Lys Gln Val Pro Lys Phe Thr Lys Asp Thr Ala Gln Leu Tyr
1 5 10 15
Thr Cys Lys Trp Leu Leu Tyr Asn Lys Val Thr Lys Met Tyr Asp His
20 25 30
Thr Val Val Asn His Ser Val Arg Glu Tyr Ile Thr Asp Ser Ile Ser
35 40 45
Thr Asn Thr Ile Glu Glu Thr Gly
50 55

(2) INFORMATION FOR SEQ ID NO:279:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 153 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

Met Lys Lys Arg Ala Ile Val Ala Val Ile Val Leu Leu Leu Ile Gly
1 5 10 15
Leu Asp Gln Leu Val Lys Ser Tyr Ile Val Gln Gln Ile Pro Leu Gly
20 25 30
Glu Val Arg Ser Trp Ile Pro Asn Phe Val Ser Leu Thr Tyr Leu Gln
35 40 45
Asn Arg Gly Ala Ala Phe Ser Ile Leu Gln Asp Gln Gln Leu Leu Phe
50 55 60
Ala Val Ile Thr Leu Val Val Val Ile Gly Ala Ile Trp Tyr Leu His
65 70 75 80
Lys His Met Glu Asp Ser Phe Trp Met Val Leu Gly Leu Thr Leu Ile
85 90 95
Ile Ala Gly Gly Leu Gly Asn Phe Ile Asp Arg Val Ser Gln Gly Phe
100 105 110
Val Val Asp Met Phe His Leu Asp Phe Ile Asn Phe Ala Ile Phe Asn
115 120 125
Val Ala Asp Asn Tyr Leu Thr Val Gly Val Ile Ile Leu Leu Ile Ala
130 135 140
Met Leu Lys Glu Glu Ile Asn Gly Asn
145 150

(2) INFORMATION FOR SEQ ID NO:280:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Met Gly Ala Tyr Tyr Leu Val Met Gln Ser Leu Ser Tyr Leu Glu Tyr
1 5 10 15
Glu Gln Gly Ile Gln Ser Thr Thr Val Arg His Leu Ile Leu Val Phe
20 25 30
Tyr Leu Leu Phe Phe Met Gly Gly Ile Lys Lys Leu Asp Thr Tyr Leu
35 40 45
Lys Glu Lys Leu Gln Glu Glu Leu Asn Gln Glu Gln Thr Leu Arg Tyr
50 55 60
Arg Asp Met Glu Arg Tyr Ser Arg His Ile Glu Glu Leu Tyr Lys Glu
65 70 75 80
Ile Arg Ser Phe Arg His Asp Tyr Thr Asn Leu Leu Thr Thr Tyr Val
85 90 95
Trp Ala Leu Lys Arg Arg Ile Trp Ser Arg
100 105

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Met His Val Arg Met Ile Pro Lys Ser Thr Pro Asp Thr Lys Phe Ala
1 5 10 15
Asp Val Ala Thr His Gln Pro Glu Tyr Ser Arg Asp Asn Val Ala Gly
20 25 30
Thr Ile Val Gly Phe Trp Thr Pro Glu Ile Phe His Gly Val Ser Val
35 40 45
Ala Gly Tyr His Leu His Phe Ile Ser Asp Asp Leu Thr Phe Gly Gly
50 55 60
His Val Met Asp Phe Val Ile Lys Glu Gly Ile Ile Glu Val Gly Ala
65 70 75 80
Val Asp Gln Leu Asp Gln Arg Phe Pro Val Gln Asp Arg Gln Tyr Leu
85 90 95
Phe Ala Lys Phe Asn Val Asp Glu Met Lys Lys Asp Ile Glu Lys Ala
100 105 110
Glu

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

Met Ala Val Ala Lys Gly Lys Leu Thr Ile Ile Ala His Val Ala Cys			
1	5	10	15
Asn Asn Thr Lys Asp Ser Met Glu Leu Ala Arg His Ala Glu Ser Leu			
20	25	30	
Gly Val Asp Ala Ile Ala Thr Asp Ser Thr Asn Leu Phe Pro Leu Ala			
35	40	45	
Arg Ile Thr Gln Leu Pro Asn Thr Gly Thr Ile Ser Val Leu Gln Leu			
50	55	60	
Gln Thr Gln Thr Thr			
65			

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

Met Gly Glu Thr Gln Ile Ile Asp Gly Leu Asp Pro Glu Tyr Lys Lys			
1	5	10	15
Arg Phe Met His His Tyr Asn Phe Pro Gln Tyr Ser Val Gly Glu Thr			
20	25	30	
Gly Arg Tyr Gly Ala Pro Gly Arg Arg Glu Ile Gly His Gly Ala Leu			
35	40	45	
Gly Glu Arg Ala Leu Ala Gln Val Leu Pro Ser Leu Glu Glu Phe Pro			
50	55	60	

Tyr Ala Ile Arg Leu Val Ala Glu Val Leu Glu Ser Asn Gly Ser Ser
65 70 75 80
Ser Gln Ala Ser Ile Cys Ala Gly Thr Leu Ala Leu Met Ala Gly Gly
85 90 95
Val Pro Ile Lys Ala Pro Val Ala Gly Ile Ala Met Gly Leu Ile Ser
100 105 110
Asp Gly Asn Asn Tyr Thr Val Leu Thr Asp Ile Gln Gly Leu Glu Asp
115 120 125
His Phe Gly Asp Met Asp Phe Lys Val Ala Gly Thr Arg Asp Gly Ile
130 135 140
Thr Ala Leu Gln Met Asp Ile Lys Ile Gln Gly Ile Thr Ala Glu Ile
145 150 155 160
Leu Thr Glu Ala Leu Ala Gln Ala Lys Lys Ala Arg Phe Glu Ile Leu
165 170 175
Asp Val Ile Glu Ala Thr Ile Pro Glu Val Arg Pro Glu Leu Ala Pro
180 185 190
Thr Ala Pro Lys Ile Asp Thr Ile Lys Ile Asp Val Asp Lys Ile Lys
195 200 205
Ile Val Ile Gly Lys Gly Glu Thr Ile Asp Lys Ile Ile Ala Glu
210 215 220
Thr Gly Val Lys Ile Asp Ile Asp Glu Glu Xaa Asn Val Phe Tyr Leu
225 230 235 240
Leu Leu Val Asp Gln Asn Ala Ile Asn Pro Cys Pro Lys Lys Leu Leu
245 250 255
Leu Val Trp Phe Arg Glu Pro Lys Trp Met Lys Phe Thr Val Leu Asn
260 265 270
Arg Ser Tyr Arg Glu Phe Gly Ala Phe Val Thr Leu
275 280

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Met Ile Asn Asn Val Val Leu Val Gly Arg Met Thr Arg Asp Ala Glu
1 5 10 15

Leu Arg Tyr Thr Pro Ser Asn Val Ala Val Ala Thr Phe Thr Leu Ala
 20 25 30
 Val Asn Arg Thr Phe Lys Ser Gln Asn Gly Glu Arg Glu Ala Asp Phe
 35 40 45
 Ile Asn Val Val Met Trp Arg Gln Gln Ala Glu Asn Leu Ala Asn Trp
 50 55 60
 Ala Lys Lys Gly Ser Leu Ile Gly Val Thr Gly Arg Ile Gln Thr Arg
 65 70 75 80
 Ser Tyr Asp Asn Gln Gln Gly Gln Arg Val Tyr Val Thr Glu Val Val
 85 90 95
 Ala Glu Asn Phe Gln Met Leu Glu Ser Arg Ser Val Arg Glu Gly His
 100 105 110
 Thr Gly Gly Ala Tyr Ser Ala Pro Thr Ala Asn Tyr Ser Ala Pro Thr
 115 120 125
 Asn Ser Val Pro Asp Phe Ser Arg Asn Glu Asn Pro Phe Gly Ala Thr
 130 135 140
 Asn Pro Leu Asp Ile Ser Xaa Asp Asp Leu Pro Phe
 145 150 155

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

Met Asp Leu Val Arg Ile Leu Lys Glu Pro Arg Asn Ala Leu Val Lys
 1 5 10 15
 Gln Tyr Gln Thr Leu Leu Ser Tyr Asp Asp Val Glu Leu Glu Phe Asp
 20 25 30
 Asp Glu Ala Leu Gln Glu Ile Ala Asn Lys Ala Ile Glu Arg Lys Thr
 35 40 45
 Gly Ala Arg Gly Leu Arg Ser Ile Ile Glu Glu Thr Met Leu Asp Val
 50 55 60
 Met Phe Glu Val Pro Ser Gln Glu Asn Val Lys Leu Val Arg Ile Thr
 65 70 75 80
 Lys Glu Thr Val Asp Gly Thr Asp Lys Pro Ile Leu Glu Thr Ala
 85 90 95

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

Met Thr Glu Ala Gly Tyr Val Gly Glu Asp Val Glu Asn Ile Leu Leu
1 5 10 15
Lys Leu Leu Gln Val Ala Asp Phe Asn Ile Glu Arg Ala Glu Arg Gly
20 25 30
Ile Ile Tyr Val Asp Glu Ile Asp Lys Ile Ala Lys Lys Ser Glu Asn
35 40 45
Val Ser Ile Thr Arg Asp Val Ser Gly Glu Gly Val Gln Gln Ala Leu
50 55 60
Leu Lys Ile Ile Glu Gly Thr Val Ala Ser Val Pro Pro Gln Gly Gly
65 70 75 80
Arg Lys His Pro Gln Gln Val Asp Asp Ser Ser Gly Tyr Lys Lys Tyr
85 90 95
Pro Leu His Arg Gly Trp Cys Phe
100

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

Met Trp Pro Arg Glu Ser Arg Ser Cys Arg Leu Thr Lys Val Lys Ile
1 5 10 15

Cys Gly Leu Ser Thr Lys Glu Ala Val Glu Thr Ala Val Ser Ala Gly
 20 25 30
 Ala Asp Tyr Ile Gly Phe Val Phe Ala Pro Ser Lys Arg Gln Val Thr
 35 40 45
 Leu Glu Glu Ala Ala Glu Leu Ala Lys Leu Ile Pro Ala Asp Val Lys
 50 55 60
 Lys Val Gly Val Phe Val Ser Pro Ser Arg Val Glu Leu Leu Glu Ala
 65 70 75 80
 Ile Asp Lys Val Gly Leu Asp Leu Val Gln Val His Gly Gln Val Ala
 85 90 95
 Asp Asp Leu Phe Glu Asn Leu Pro Cys Ala Ser Ile Gln Ala Val Gln
 100 105 110
 Val Asp Gly Asn Gly His Val Pro Asn Ser Gln Ala Asp Tyr Leu Leu
 115 120 125
 Phe Asp Ala Pro Val Ala Gly Ser Gly Gln Ser Phe Asp Trp Gly Gln
 130 135 140
 Leu Asp Thr Thr Gly Leu Ala Gln Pro Phe Phe Ile Ala Gly Gly Leu
 145 150 155 160
 Asn Glu Asp Asn Val Val Lys Ala Ile Gln His Phe Thr Pro Tyr Ala
 165 170 175
 Val Asp Val Ser Ser Gly Val Glu Thr Asp Gly Gln Lys Asp His Glu
 180 185 190
 Lys Ile Arg Arg Phe Ile Glu Arg Val Lys His Gly Ile Ser Gly Thr
 195 200 205
 Lys

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

Met Asn Cys Glu Ala Val Ala Leu Gly Ser Phe Cys Glu Leu Lys Ser
 1 5 10 15
 Arg Arg Gly Lys Lys Gln Lys Gly Glu Ile Leu Met Ala Val Ile Ser
 20 25 30

Met Lys Gln Leu Leu Glu Ala Gly Val His Phe Gly His Gln Thr Arg
35 40 45
Arg Trp Asn Pro Lys Met Ala Lys Tyr Ile Phe Thr Glu Arg Asn Gly
50 55 60
Ile His Val Ile Asp Leu Gln Gln Thr Val Lys Tyr Ala Asp Gln Ala
65 70 75 80
Tyr Xaa Phe Met Arg Asp Ala Ala Asn Asp Ala Val Val Leu Phe
85 90 95
Val Gly Thr Lys Lys Thr Ser Ser
100

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

Met Val Asp Thr Asn Thr Asp Pro Asp Asp Ile Asp Val Ile Ile Pro
1 5 10 15
Ala Asn Asp Asp Ala Ile Arg Ala Val Lys Leu Ile Thr Ala Lys Leu
20 25 30
Ala Asp Ala Ile Ile Glu Gly Arg Gln Gly Glu Asp Ala Val Ala Val
35 40 45

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

Met Glu Glu Leu Gly Gln Ser Tyr Gly Tyr Leu Leu Tyr Arg Thr Glu
1 5 10 15

Thr Asn Trp Asp Ala Glu Glu Arg Leu Arg Ile Ile Asp Gly Arg
 20 25 30
 Asp Arg Ala Gln Leu Tyr Val Asp Gly Gln Trp Val Lys Thr Gln Tyr
 35 40 45
 Gln Thr Glu Ile Gly Glu Asp Ile Phe Tyr Gln Gly Lys Lys Lys Gly
 50 55 60
 Leu Ser Arg Leu Asp Ile Leu Ile Glu Asn Met Gly Arg Val Asn Tyr
 65 70 75 80
 Gly His Lys Phe Leu Ala Asp Thr Gln Arg Lys Gly Ile Arg Thr Gly
 85 90 95
 Val Cys Lys Asp Leu His Phe Leu Leu Asn Trp Lys His Tyr Pro Leu
 100 105 110
 Pro Leu Asp Asn Pro Glu Lys Ile Asp Phe Ser Lys Gly Trp Thr Gln
 115 120 125
 Gly Gln Pro Ala Phe Tyr Ala Tyr Asp Phe Thr Val Glu
 130 135 140

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

Met Gly Lys Glu Lys Val Trp Leu Pro Arg Lys Gln Gly Leu Pro Gly
 1 5 10 15
 Leu Ala Tyr Tyr Val Ile Glu Val Ala His Lys Glu Glu Leu Leu Thr
 20 25 30
 Ile Ala Gln Arg Ala Gln Glu Val Asp Val Pro Ile Lys Trp Met Thr
 35 40 45
 Ser Ser Gln Leu Glu Ile Thr Asp Ser Asp Gly Ile Val Thr Cys Ile
 50 55 60
 Arg Leu Ala Arg
 65

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

Met Asn Lys Lys Gln Trp Leu Gly Leu Gly Leu Val Ala Val Ala Ala
1 5 10 15
Val Gly Leu Ala Ala Cys Gly Asn Arg Ser Ser Arg Asn Ala Ala Ser
20 25 30
Ser Ser Asp Val Lys Thr Lys Ala Ala Ile Val Thr Asp Thr Gly Gly
35 40 45
Val Asp Asp Lys Ser Phe Asn Gln Ser Ala Trp Glu Val Ala Gly Leu
50 55 60
Gly
65

(2) INFORMATION FOR SEQ ID NO:293:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

Met Ser Gln Trp Asp Arg Lys Leu Asp Ala Arg Leu Ala Gln Ala Val
1 5 10 15
Val Ser Ile Asn Ala Phe Lys Gly Val Glu Phe Gly Leu Gly Phe Glu
20 25 30
Ala Gly Tyr Arg Lys Gly Ser Gln Val Met Asp Glu Ile Leu Trp Ser
35 40 45
Lys Glu Asp Gly Tyr Thr Arg Arg Thr Asn Asn Leu Gly Gly Phe Glu
50 55 60
Gly Gly Met Thr Asn Gly Gln Pro Ile Val Val Arg Gly Val Met Lys
65 70 75 80
Pro Ile Pro Thr Leu Tyr Lys Pro Leu Met Ser Val Asp Ile Glu Thr
85 90 95

His Glu Pro Tyr Lys Ala Thr Val Glu Arg Ser Asp Pro Thr Ala Leu
100 105 110
Pro Ala Ala Gly Met Val Met Glu Ala Val Val Ala Thr Val Leu Ala
115 120 125
Gln Glu Ile Leu Glu Lys Phe Ser Ser Asp Asn Leu Glu Glu Leu Lys
130 135 140
Glu Ala Val Ala Lys His Arg Asp Tyr Thr Lys Asn Tyr
145 150 155

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Met Glu Asp Ser Asn Ser Phe Met Leu Ser His Gln Met Glu Thr Ile
1 5 10 15
Leu Lys Glu Ala Gly Phe Thr Lys Ala Val Ser Tyr Phe Ile Leu Glu
20 25 30
Leu Lys Asp Pro Ser Gln Thr Lys Val Val Thr Glu Glu Leu Gln Lys
35 40 45
Asn Lys Lys Tyr Thr Val Leu Ser
50 55

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

Met Gly Lys Lys Arg Trp Ala Arg Asn Gly Phe Glu Ser Asn Asp Ala
1 5 10 15

Ser Tyr Ala Gln Val Val Ser Leu Tyr Asp Asp Thr Ser Ile Ser Val
20 25 30
Ser Asn Asn Glu Thr Asp Lys Val Leu Ala Gly Ser Leu Tyr Thr Asp
35 40 45
Thr Asn Glu Gln Gly Leu Thr Ile Pro Ser Ser Phe Thr Lys Lys Leu
50 55 60
Glu
65

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

Met Ala Met Glu Ser Gly Ala Thr Ala Val Val Ala Glu Arg Gly Gln
1 5 10 15
Glu Arg Ile Thr Lys Val Arg Glu Ile Leu Gly Gly Ala Asp Ala
20 25 30
Ala Leu Glu Cys Val Gly Thr Glu Ala Ala Ile Glu Gln Ala Leu Gly
35 40 45
Val Leu His Asn Gly Gly Arg Met Gly Phe Val Gly Val Pro His Tyr
50 55 60
Asn Asn Arg Ala Leu Gly Ser Thr Phe Met Gln Asn Ile Ser Val Ala
65 70 75 80
Gly Gly Ala Ala Ser Ala Thr Thr Tyr Asp Lys Gln Phe Leu Leu Lys
85 90 95
Ala Val Leu Asp Gly Asp Ile Asn Pro Gly Arg Val Phe Thr Ser Ser
100 105 110
Tyr Lys Leu Glu Asp Ile Asp Gln Ala Tyr Lys Asp Met Asp Glu Arg
115 120 125
Lys Thr Ile Lys Ser Met Ile Val Ile Glu
130 135

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

Met Lys Gln Val Val Asp Tyr Phe Leu Ser Gln Gly Met Asp Arg Ile
1 5 10 15
Gly Ile Leu Thr Gly Leu Glu Glu Thr Thr Asp Gln Glu Glu Ile Ile
20 25 30
Gln Asp Lys Arg Leu Glu Asn Phe Lys Asn Tyr Ser Gln Ala Arg Gly
35 40 45
Ile Tyr His Asp Glu Leu Val Phe Gln Gly Arg Phe Thr Ala Gln Ser
50 55 60
Gly Tyr Asp Leu Met Lys Glu Ala Ile Gln Ser Leu Gly Asp Gln Leu
65 70 75 80
Pro Pro Ala Phe Phe Ala Ala Ser Asp Ser Leu Ala Ile Gly Ala Leu
85 90 95
Arg Ala Leu Gln Glu Ala Gly Ile Ser Leu Pro Asp Arg Val Ser Leu
100 105 110
Ile Phe Leu Leu Thr Thr Leu Ser Leu Thr Lys Gln Val Tyr Pro Pro
115 120 125
Leu Ser
130

(2) INFORMATION FOR SEQ ID NO:298:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

Met Ala Lys Val Thr Ile Met Leu Ala Cys Ala Ala Gly Met Ser Thr
1 5 10 15
Ser Leu Leu Val Thr Lys Met Gln Lys Ala Ala Glu Asp Lys Gly Leu
20 25 30

WO 97/37026

Asp Ala Glu Ile Phe Ala Val Pro Ala Pro Glu Ala Glu Glu Ile Val		
35	40	45
Ala Thr Lys Glu Val Asn Val Leu Leu Leu Gly Pro Gln Val Arg Tyr		
50	55	60
Leu Leu Gly Asp Phe Gln Glu Lys Leu Lys Asp Arg Gln Ile Pro Val		
65	70	75
Ala Val Ile Pro Met Thr Asp Tyr Gly Met Met Asn Gly Ser Lys Val		
85	90	95
Leu Asp Leu Ala Glu Ser Leu Leu Asp		
100	105	

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

Met His Gly Ala Gly Val Asn Glu Pro Val Ala Glu Leu Ser Val Ala		
1	5	10
Glu Gln Leu Leu Glu Ala Gly Ala Asp Val Ile Leu Val Pro Ala Val		
20	25	30
Gly Thr Val Pro Ala Phe His Asp Gln Glu Leu Arg Glu Val Val Asp		
35	40	45
Leu Val His Ser Lys Gly Gly Leu Val Leu Ser Ala Ile Gly Thr Ser		
50	55	60
Gln Glu Thr Ser Asp Thr Asp Thr Ile Lys Glu Ile Ala Leu Arg Asn		
65	70	75
Lys Ile Cys Gly Val Asp Ile Gln His Ile Gly Asp Ala Gly Tyr Gly		
85	90	95
Gly Leu Ala Thr Val Asp Asn Ile Tyr Ala Leu Ser Lys Ala Ile Arg		
100	105	110
Gly Val Arg His Thr Val Ser Arg Leu Ala Arg Ser Val Asn Arg		
115	120	125

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

Met Ser Ala Ile Asn Leu Ala Ser Val Pro Lys Glu Ser Leu Thr Gln
1 5 10 15
Val Leu Pro Arg Asp Leu His Ala Glu Tyr Phe Ala Val Leu Ala Ser
20 25 30
Ile Ala Thr Ser Ile Glu Arg Met Ala Thr Glu Ile Arg Gly Leu Gln
35 40 45
Lys Ser Glu Gln Arg Glu Val Glu Glu Phe Phe Ala Lys Gly Gln Lys
50 55 60
Gly Ser Ser Ala Met Pro His Lys Arg Asn Pro Ile Gly Ser Glu Asn
65 70 75 80
Met Thr Gly Leu Ala Arg Val Ile Arg Gly His Met Ile Thr Ala Tyr
85 90 95
Glu Asn Val Ala Leu Trp His Glu Arg Asp Ile Ser His Ser Ser Ala
100 105 110
Glu Arg Ile Ile Thr Pro Asp Thr Thr Ile Leu Ile Asp Tyr Met Leu
115 120 125
Asn Arg Phe Gly Asn Ile Val Lys Asn Leu Thr Val Phe Pro Glu Asn
130 135 140
Met Ile Arg Asn Met Asn Ser Thr Phe Gly Leu Ile Phe Ser Gln Arg
145 150 155 160
Ala Met Leu Thr Leu Ile Glu Lys Gly Met Thr Arg Glu Gln Ala Tyr
165 170 175
Asp Leu Val Gln Pro Lys Thr Ala Tyr Ser Trp Asp Asn Gln Val Asp
180 185 190
Phe Lys Pro Leu Leu Glu Ala Asp Ser Glu Val Thr Ser Arg Leu Thr
195 200 205
Gln Glu Glu Ile Asp Glu Ile Phe Asn Pro Val Tyr Thr Lys Arg
210 215 220
Val Asp Asp Ile Phe Glu Arg Leu Gly Leu Gly Asp
225 230 235

(2) INFORMATION FOR SEQ ID NO:301:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

Met Leu Asn Leu Thr His Val Thr Leu Lys Thr Arg Gln Val Ile Leu
1 5 10 15
Gln Asp Ala Asp Phe Thr Phe Lys Lys Gly Arg Ile Tyr Gly Leu Leu
20 25 30
Ala Ile Asn Gly Ser Gly Lys Thr Thr Leu Phe Arg Ala Met Ser Lys
35 40 45
Leu Leu Pro Leu Ser Ser Gly His Ile Ala Val Pro Pro Ser Leu Phe
50 55 60
Tyr Tyr Glu Ser Val Glu Trp Leu Asp Gly Asn Leu Ser Gly Met Asp
65 70 75 80
Tyr Leu Arg Leu Ile Lys Lys His Leu Glu Val Arg Pro Lys Leu Glu
85 90 95
Arg

(2) INFORMATION FOR SEQ ID NO:302:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

Met Tyr Thr Leu Gly Gln Pro Asn Glu Leu Ala Ala Glu Phe Leu Asn
1 5 10 15
Phe Val Leu Ser Asp Glu Thr Gln Glu Gly Ile Val Lys Gly Leu Lys
20 25 30
Tyr Ile Pro Ile Lys Glu Met Lys Val Glu Lys Asp Ala Ala Gly Thr
35 40 45
Val Thr Val Leu Glu Gly Arg Gln
50 55

(2) INFORMATION FOR SEQ ID NO:303:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 187 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

```

Met Asn Gln Glu Glu Leu Ala Lys Lys Met Leu Leu Pro Ser Lys Asn
 1           5           10           15
Ser Arg Leu Glu Lys Leu Gly Lys Gly Leu Thr Phe Ala Cys Leu Ser
 20          25           30
Leu Ile Val Ile Leu Val Ala Met Ile Leu Val Phe Val Ala Gln Lys
 35          40           45
Gly Leu Ser Thr Phe Phe Val Asn Gly Val Asn Ile Phe Asp Phe Leu
 50          55           60
Leu Gly Gly Thr Trp Asn Pro Ser Ser Lys Glu Phe Gly Ala Leu Pro
 65          70           75           80
Met Ile Leu Gly Ser Phe Ile Val Thr Ile Leu Ser Ala Leu Ile Ala
 85          90           95
Thr Pro Phe Ala Ile Gly Ala Ala Val Phe Met Thr Glu Val Ser Pro
100         105          110
Lys Gly Ala Lys Ile Leu Gln Pro Ala Ile Glu Leu Leu Val Gly Ile
115         120          125
Pro Ser Val Val Tyr Gly Phe Ile Gly Leu Gln Val Val Val Pro Phe
130         135          140
Val Arg Ser Val Phe Gly Gly Thr Gly Phe Gly Ile Leu Ser Gly Ile
145         150          155          160
Ser Val Leu Phe Val Met Ile Leu Pro Thr Val Thr Phe Met Thr Thr
165         170          175
Asp Ser Leu Arg Ala Val Pro Xaa Leu Leu Ser
180         185

```

(2) INFORMATION FOR SEQ ID NO:304:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 242 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

Met Thr Glu Ile Arg Leu Glu His Val Ser Tyr Ala Tyr Gly Gln Glu
1 5 10 15
Arg Ile Leu Glu Asp Ile Asn Leu Gln Val Thr Ser Gly Glu Val Val
20 25 30
Ser Ile Leu Gly Pro Ser Gly Val Gly Lys Thr Thr Leu Phe Asn Leu
35 40 45
Ile Ala Gly Ile Leu Glu Val Gln Ser Gly Arg Ile Val Leu Asp Gly
50 55 60
Glu Glu Asn Pro Lys Gly His Val Ser Tyr Met Leu Gln Lys Asp Leu
65 70 75 80
Leu Leu Glu His Lys Thr Val Leu Gly Asn Ile Ile Leu Pro Leu Leu
85 90 95
Ile Gln Lys Val Asp Lys Ala Glu Ala Ile Ser Arg Ala Asp Lys Ile
100 105 110
Leu Ala Thr Phe Gln Leu Thr Ala Val Arg Asp Lys Tyr Pro His Glu
115 120 125
Leu Ser Gly Gly Met Arg Gln Arg Val Ala Leu Leu Arg Thr Tyr Leu
130 135 140
Phe Gly His Lys Leu Phe Leu Leu Asp Glu Ala Phe Ser Ala Leu Asp
145 150 155 160
Glu Met Thr Lys Met Glu Leu His Ala Trp Tyr Leu Glu Ile His Lys
165 170 175
Gln Leu Gln Leu Thr Thr Leu Ile Xaa Thr His Ser Ile Glu Glu Ala
180 185 190
Leu Xaa Leu Ser Asp Arg Ile Tyr Ile Leu Xaa Asn Xaa Pro Gly Gln
195 200 205
Ile Val Ser Glu Ile Lys Leu Asp Trp Ser Glu Asp Glu Asp Xaa Glu
210 215 220
Val Xaa Lys Ile Ala Xaa Lys Arg Gln Ile Leu Ala Glu Leu Gly Leu
225 230 235 240
Asp Lys

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

Met Glu His Pro Xaa Glu Ala Ala Asp Ile Leu Ile Lys Asn Ala Pro
1 5 10 15
Glu Leu Lys Glu Lys Arg Asp Phe Val Ile Glu Ser Gln Lys Tyr Leu
20 25 30
Ser Lys Glu Tyr Ala Ser Asp Lys Glu Lys Trp Gly Gln Phe Asp Ala
35 40 45
Ala Arg Trp Asn Ala Phe Tyr Lys Trp Asp Lys Glu Asn Gly Ile Leu
50 55 60
Lys Glu Asp Leu Thr Asp Lys Gly Phe Thr Asn Glu Phe Val Lys
65 70 75

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Met Val Tyr Thr Ser Leu Ser Ser Lys Asp Gly Asn Tyr Pro Tyr Gln
1 5 10 15
Leu Asn Ile Ala His Leu Tyr Gly Asn Leu Met Asn Thr Tyr Gly Asp
20 25 30
Asn Gly Asn Ile Leu Met Leu Lys Tyr Val Ala Glu Lys Leu Gly Thr
35 40 45
His Val Thr Val Asp Ile Val Ser Leu His Asp Asp Phe Asp Glu Asn
50 55 60
His Tyr Asp Ile Ala Phe Phe Gly Gly Gln Asp Phe Glu Gln Ser
65 70 75 80
Ile Ile Ala Asp Asp Leu Pro Ala Lys Lys Glu Ser Ile Asp Asn Tyr
85 90 95
Ile Gln Asn Asp Gly Val Val Leu Ala Ile Cys Gly Phe Gln Leu
100 105 110
Leu Gly Gln Tyr Tyr Val Glu Ala Ser Gly Lys Arg Ile Glu Gly Leu
115 120 125

Gly Val Met Gly His Tyr Thr Leu Asn Gln Thr Asn Asn Arg Phe Ile
130 135 140
Gly Asp Ile Lys Ile His Asn Glu Arg Phe Arg
145 150 155

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

Met His Gln His Ser Pro His Thr Ala Ser Tyr Thr Ser Ser Arg Asp
1 5 10 15
Ala Met Ser Lys Tyr Pro Glu Arg Cys Thr Thr Val Gly Leu Arg Leu
20 25 30
Asn Glu Glu Ser Asp Phe Glu Leu Tyr Ala Pro Tyr Gly Leu Glu Asp
35 40 45
Ile Leu Asn Phe Lys Phe Val Gln Leu Leu Ile Ser
50 55 60

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

Met Phe Glu Ile Phe Asn Met Gly Val Gly Leu Met Leu Ala Val Ser
1 5 10 15
Pro Glu Asn Val Glu Arg Val Lys Glu Leu Leu Asp Glu Ala Val Tyr
20 25 30
Glu Ile Gly Arg Ile Val Lys Lys Glu Asn Glu Ser Val Ile Ile Lys
35 40 45

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

Met	Met	Val	Lys	Lys	His	Tyr	Phe	Lys	Asp	Asn	Glu	Glu	Asp	Ser	Lys
1								5			10				15
Met	Arg	Arg	Ile	Leu	Leu	Leu	Val	Ala	Val	Leu	Leu	Met	Ile	Pro	Ser
												20		25	30
Phe	Ile	Ser	Ala	Thr	Thr	Leu	Val	Arg	Glu	Thr	Leu	Lys	Lys	Glu	Ser
								35		40				45	
Leu	Lys	Lys	Phe	Ile	Ser	Glu	Gln	Phe	Gly	His	Asn	Ile	Leu	Lys	
						50		55			60				
Lys	Thr	Tyr	Ser	Lys	Lys	Thr	His	Thr	Leu	Lys	Leu	Thr	Ile	Ser	Gly
						65		70		75			80		
Asn	Tyr	Leu	Thr	Glu	Glu	Leu	Asp	Met	Ile	Ser	Ser	Lys	Arg	Gly	
						85			90			95			
Asp	Tyr	Gly	Leu	Ser	Asp	Val	Ser	Val	Gln	Val	Ser	Gln	Leu	Ser	Asp
						100			105			110			
Ser	Glu	Gln	Leu	Ser	Lys	Glu	Glu	Leu	Val	Glu	Tyr	Phe	Phe	Gln	Tyr
						115			120			125			
Ile	Lys	Asp	Lys	Glu	Ala	Lys	Glu	Lys	Glu	Lys	Ala	Asn	Lys	Phe	Tyr
						130		135			140				
Thr	Glu	Ser	Glu	Glu	Gln										
						145		150							

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

Met Ser Ile Glu Pro Arg Arg Arg Trp Arg Asn Ser Thr Val Cys Leu
1 5 10 15
Glu Ala Glu Leu Tyr Gln Glu Ser Leu Val Leu Ile Gly Gly Asp Pro
20 25 30
Gly Ile Gly Lys Ser Thr Leu Leu Leu Gln Val Ser Thr Gln Leu Ser
35 40 45
Gln Val Gly Thr Val Leu Tyr Val Ser Gly Glu Glu Ser Ala Gln Gln
50 55 60
Ile Lys Leu Arg Ala Glu Arg Leu Gly Asp Phe Asp Ser Glu Phe Tyr
65 70 75 80
Leu Tyr Ala Glu Thr Asn Met Gln Ser Val Arg Ala Glu Val Val Ala
85 90 95
Tyr Pro Ala Arg Leu Ser His Tyr
100

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

Met Ala Thr Lys Gln Lys Glu Val Thr Thr Phe Asp Val Gln Val Ala
1 5 10 15
Glu Phe Ile Arg Asn His Lys Gln Lys Gly Thr Ala Thr Asp Asp Glu
20 25 30
Ile Asn Ala Ser Leu Val Ile Pro Phe Thr Leu Asp Ala Asp Gly Ile
35 40 45
Glu Asp Leu Leu Gln Arg Ile Gln Asp Ala Gly Ile Ser Ile Thr Asp
50 55 60
Asn Glu Gly Asn Pro Ser Ala Arg Val Leu Ser Asn Glu Glu Pro
65 70 75 80
Glu Leu Ser Asp Glu Asp Leu Ile Gly Ser Thr Ser Ala Lys Val Asn
85 90 95
Asp Pro Val Arg Met Tyr Leu Lys Glu Ile Gly Val Val Pro Leu Leu
100 105 110

Thr Asn Glu Glu Glu Lys Glu Leu Ala Leu Ala Val Glu Ala Gly Asp
 115 120 125
 Ile Glu Ala Lys Gln Arg Leu Ala Glu Ala Asn Leu Arg Leu Val Val
 130 135 140
 Ser Ile Ala Lys Arg Tyr Val Gly Arg Gly Xaa Gln Ser Leu Thr
 145 150 155

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

Met Met Leu Lys Pro Ser Ile Asp Thr Leu Leu Asp Lys Val Pro Ser
 1 5 10 15
 Lys Tyr Ser Leu Val Ile Leu Glu Ala Lys Arg Ala His Glu Leu Glu
 20 25 30
 Ala Gly Ala Pro Ala Thr Gln Gly Phe Lys Ser Glu Lys Ser Thr Leu
 35 40 45
 Arg Ala Leu Glu Glu Ile Glu Ser Gly Asn Val Thr Ile His Pro Asp
 50 55 60
 Pro Glu Gly Lys Arg Glu Ala Val Arg Arg Arg Ile Glu Glu Glu Lys
 65 70 75 80
 Arg Arg Lys Glu Glu Glu Lys Lys Ile Lys Glu Gln Ile Ala Lys
 85 90 95
 Glu Lys Glu Asp Gly Glu Lys Ile
 100

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

Met Ile Arg Gln Gly Gln Met Leu Glu Tyr Ala Glu Tyr Val Gly Asn
1 5 10 15
Tyr Tyr Gly Thr Pro Leu Thr Tyr Val Asn Glu Thr Leu Asp Lys Gly
20 25 30
Ile Asp Val Phe Leu Glu Ile Glu Val Gln Gly Ala Leu Gln Val Lys
35 40 45
Lys Lys Val Pro Asp Ala Val Phe Ile Phe Leu Thr Pro Pro Asp Leu
50 55 60
Asp Glu Leu Gln Glu Arg Leu Val Gly Arg Gly Thr Asp Ser Ala Glu
65 70 75 80
Val Ile Ala Gln Arg Ile Glu Lys Ala Lys Glu Glu Ile Ala Leu Met
85 90 95
Arg Glu Tyr Asp Tyr Ala Ile Val Asn Asp Gln Val Pro Leu Ala Ala
100 105 110
Glu Arg Val Lys Cys Val Ile Glu Ala Glu His Phe Cys Val Asp Arg
115 120 125
Val Ile Gly His Tyr Gln Glu Met Leu Pro Lys Ser Pro Thr Thr Arg
130 135 140

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

Met Ser Arg Leu Leu Val Ile Gly Cys Gly Gly Val Ala Gln Val Ala
1 5 10 15
Ile Ser Lys Ile Cys Gln Asp Ser Glu Thr Phe Thr Glu Ile Met Ile
20 25 30
Ala Ser Arg Thr Lys Ser Lys Cys Asp Asp Leu Lys Ala Lys Leu Glu
35 40 45
Gly Lys Thr Ser Thr Lys Ile Glu Thr Ala Ala Leu Asp Ala Asp Lys
50 55 60
Val Glu Glu Val Ile Ala Leu Ile Glu Ser Leu Gin Thr Ser Lys Leu
65 70 75 80
Phe

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

Met His Glu Ser Phe His Val Asp Asp Pro Thr Leu Tyr Ser Arg Glu
1 5 10 15
Trp Phe Ser Trp Ala Asn Met Met Phe Cys Glu Leu Val Leu Asp Tyr
20 25 30
Leu Asp Ile Arg
35

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

Met Arg Phe Tyr Phe Met Glu Asn Val Val Val His Ile Ile Ser His
1 5 10 15
Ser His Trp Asp Arg Glu Trp Tyr Leu Pro Phe Glu Ser His Arg Met
20 25 30
Gln Leu Val Glu Leu Phe Asp Asn Leu Phe Asp Leu Phe Glu Asn Asp
35 40 45
Pro Glu Phe Lys Ser Phe His Leu Asp Gly Gln Thr Ile Val Leu Asp
50 55 60
Asp
65

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

Met	Leu	Leu	Tyr	Ile	Leu	Ser	His	Ile	Ala	Thr	Gly	Ile	Val	Ser	Gly
1					5				10					15	
Thr	Cys	Leu	Leu	Lys	Ala	Ile	Val	Cys	Asn	Trp	Trp	Asn	Cys	Leu	Thr
						20			25					30	
Ile	Ser	Leu	Ile	Ser	Leu	Lys	Met	Thr	Leu	Ser	Ser	Arg	Val	Ser	Thr
						35			40			45			
Trp	Met	Asp	Lys	Leu	Leu	Ser	Leu	Thr	Thr	Asn	Leu	Gln	Ile	Arg	Pro
						50			55			60			
Glu	Asn	Arg	Asp	Lys	Val	Gln	Arg	Tyr	Ile	Asp	Glu	Gly	Lys	Leu	Lys
					65			70			75			80	
Ile	Gly	Pro	Phe	Tyr	Ile	Leu	Gln	Asp	Asp	Tyr	Leu	Ile	Ser	Ser	Glu
					85			85			90			95	
Ala	Asn	Val	Arg	Asn	Thr	Leu	Ile	Gly	Gln	Gln	Glu	Ala	Ala	Lys	Trp
					100			100			105			110	
Gly	Lys	Ser	Thr	Gln	Ile	Gly	Tyr	Phe	Pro	Asp	Thr	Phe	Gly	Asn	Met
					115			115			120			125	
Gly	Gln	Ala	Pro	Gln	Ile	Leu	Gln	Lys	Ser	Gly	Ile	His	Val	Ala	Ala
					130			130			135			140	
Phe	Gly	Arg	Gly	Val	Lys	Pro	Ile	Gly	Phe	Asp	Asn	Gln	Val	Leu	Glu
					145			145			150			155	
Asp	Glu	Gln	Phe	Thr	Ser	Gln	Phe	Ser	Glu	Met	Tyr	Trp	Gln	Gly	Val
						165			165			170			175
Asp	Gly	Ser	Arg	Val	Leu	Gly	Ile	Leu	Phe	Ala	Asn	Trp	Tyr	Ser	Asn
					180			180			185			190	
Gly	Asn	Glu	Ile	Pro	Val	Asp	Lys	Asp	Glu	Ala	Leu	Thr	Phe	Trp	Lys
					195			195			200			205	
Gln	Lys	Leu	Ser	Asp	Val	Arg	Cys	Leu	Arg	Phe	Asp	Gln	Pro	Met	Val
					210			210			215			220	
Asp	Asp	Glu	Thr	Ala	Val	Asn	Thr	Ser	Leu	Ser	Gln	Lys	Lys	Ser	Glu
					225			225			230			235	
Arg	Ser	His	Ser	Val	Trp	Gln	Met	Asn	Ser	Ser	Arg	Met			
						245					250				

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

Met Thr Ile Val Gly Cys Arg Ile Asp Gly Arg Leu Ile His Gly Gln
1 5 10 15
Val Ala Asn Leu Trp Ala Gly Lys Leu Asn Val Ser Arg Ile Met Val
20 25 30
Val Asp Asp Glu Val Val Asn Asn Asp Ile Glu Lys Ser Gly Leu Lys
35 40 45
Leu Ala Thr Pro Pro Gly Val Lys Leu Ser Ile Leu Pro Val Glu Lys
50 55 60
Ala Ala Ala Asn Ile Leu Ala Gly Lys Tyr Asp Ser Gln Arg Leu Phe
65 70 75 80
Ile Val Ala Arg Lys Pro Asp Arg Phe Pro Trp Phe Gly Arg Ser Arg
85 90 95
Cys Thr Thr

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

Met Ile Gln His Pro Arg Ile Gly Ile Arg Pro Thr Ile Asp Gly Arg
1 5 10 15
Arg Gln Gly Val Arg Glu Ser Leu Glu Val Gln Thr Met Asn Met Ala
20 25 30
251

Lys	Ser	Val	Ala	Asp	Leu	Ile	Ser	Ser	Thr	Leu	Lys	Tyr	Pro	Asp	Gly
35							40				45				
Glu	Pro	Val	Glu	Cys	Val	Ile	Ser	Pro	Ser	Thr	Ile	Gly	Arg	Val	Pro
50							55				60				
Glu	Ala	Ala	Ala	Ser	His	Glu	Leu	Phe	Lys	Lys	Ser	Asn	Val	Cys	Ala
65						70			75			80			
Thr	Ile	Thr	Val	Thr	Pro	Cys	Trp	Cys	Tyr	Gly	Ser	Glu	Thr	Met	Asp
						85			90			95			
Met	Ser	Pro	Asp	Ile	Pro	His	Ala	Ile	Trp	Gly	Phe	Asn	Gly	Thr	Glu
						100			105			110			
Arg	Pro	Gly	Ala	Val	Tyr	Leu	Ala	Ala	Val	Leu	Ala	Ser	His	Ala	Gln
						115			120			125			
Lys	Gly	Ile	Pro	Ala	Phe	Gly	Ile	Tyr	Gly	Arg	Asp	Val	Gln	Glu	Ala
						130			135			140			
Asn	Asp	Thr	Asp	Ile	Pro	Glu	Asp	Val	Lys	Glu	Asn	Phe			
						145			150			155			

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

Met	Leu	Leu	Ser	Thr	Lys	Gly	Ile	Glu	Glu	Gln	Glu	Ile	Ala	Arg	Pro
1							5			10			15		
Thr	Leu	Glu	Arg	Leu	Phe	Ser	Met	Arg	Glu	Asn	Tyr	Lys	Val	Thr	Gly
							20			25			30		
Arg	His	Pro	Gly	Tyr	Arg	Lys	Tyr	Asn	Gly	Asp	Gly	Ser	Met	Lys	Glu
							35			40			45		
Thr	Glu	Lys													
							50								

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

Met Leu Thr Leu Thr Pro Asp Val Ile Tyr Gln Glu Pro Asp Ile Leu
1 5 10 15
Tyr Gln His Glu Asp Phe Ser Leu Val Lys Ile Arg Gln Ile Arg Phe
20 25 30
Cys

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

Met Ser Ser Val Val Gly Leu Met Gly Asn Ile Gly Gln Ala Asn Tyr
1 5 10 15
Ala Ala Ser Lys Ala Gly Leu Ile Gly Phe Thr Lys Ser Val Ala Arg
20 25 30
Glu Val Ala Ser Arg Asn Ile Arg Val Asn Val Ile Ala Pro Gly Asn
35 40 45
Asp

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

Met Lys Leu Glu His Lys Asn Ile Phe Ile Thr Gly Ser Ser Arg Gly
1 5 10 15
Ile Gly Leu Ala Ile Ala His Lys Phe Ala Gln Ala Gly Ala Asn Ile
20 25 30
Val Leu Asn Ser Arg Gly Ala Ile Ser Glu Glu Leu Leu Ala Glu Phe
35 40 45
Ser Asn Tyr Gly Ile Lys Val Val Pro Ile Ser Gly Asp Val Ser Asp
50 55 60
Phe Ala Asp Ala Lys Arg Met Ile Asp Gln Ala Ile Ala Glu Leu Gly
65 70 75 80
Ser Val Asp Val Leu Val Asn Asn Ala Gly Ile Thr Gln Asp Thr Leu
85 90 95
Met Leu Lys Met Thr Glu Ala Asp Phe Glu Lys Val Leu Lys Val Asn
100 105 110
Leu Thr Gly Ala Phe Asn Met Thr Gln Ser Val Phe Gly Asn Arg
115 120 125

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

Met Glu Ser Met Pro Arg Ile Gly Leu Leu Val Thr Val Glu Asn Arg
1 5 10 15
Asp Thr Glu Thr Ile Phe Asn Ala Ala Gly Leu Asp Phe Asp Val Leu
20 25 30
Lys Ala Ser Ala Ile Ala Tyr Ile Asn Ala Asn Thr Phe Val Gln Lys
35 40 45
Glu Asn Ala Gly Glu Met Gly Arg Ser Val Ser Tyr His Asp Met Arg
50 55 60
Ser Val
65

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

Met	Arg	Gln	Gly	Gln	Gly	Ser	Val	Glu	Ala	Ile	Phe	Asn	Ala	Ile	Asp
1							5			10					15
Lys	Phe	Phe	Asn	Gln	Ser	Val	Arg	Leu	Val	Ser	Tyr	Thr	Ile	Asn	Ala
							20			25					30
Val	Thr	Asp	Gly	Ile	Asp	Ala	Gln	Asp	Arg	Val	Val	Gly	His	Cys	
							35			40					45

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

Met	Val	Glu	Asn	Pro	Glu	Gly	Phe	His	Phe	Asp	Asp	Leu	Gln	Leu	Gln
1							5			10					15
Thr	His	Ala	Asp	Asn	Asp	Ile	Glu	Ala	Leu	Val	Ser	Leu	Ala	Asn	Met
							20			25					30
Asp	Gly	Glu	Lys	Val	Glu	Phe	Asn	Ala	Thr	Gly	Thr	Gly	Phe	Arg	
							35			40					45

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

Met Asn Phe Gln Leu Ala Lys Tyr Ser Leu Leu Lys Phe Ser Glu
1 5 10 15
Asn Ile Gly Phe Thr Thr Pro Glu Glu Cys Gly Ala Ile Phe Gln Tyr
20 25 30
Leu Ile Glu Asn Val Gln Thr Asp Arg Gln Ile Ile Tyr Ser Pro Pro
35 40 45
Cys His Asp Glu Leu Arg Met Ala Val Ala Asn Ser Leu Ala Ala Val
50 55 60
Lys Asn Gly Ala Gly Leu Phe Glu Glu Thr Ile His Gly Ile Arg Glu
65 70 75 80
Arg Ala Glu Asn Ala Ala Leu Glu Glu Ile Ala Val Ala Leu Asn Ile
85 90 95
Arg Gln Asp Tyr Tyr Gln Val Glu Thr Ser Ile Val Leu Asn Glu Thr
100 105 110
Ile Asn Thr Ser Glu Met Val Ser Arg Phe Ser Gly Ile Pro Val Pro
115 120 125
Lys Asn Lys Ala Val Val Gly Gly Asn Thr Phe Ser His Glu Ser Gly
130 135 140
Ile His Gln Asp Gly Val Leu Lys Asn Pro Leu Thr Tyr Glu Ile Ile
145 150 155 160
Thr Pro Glu Leu Val Gly Val Lys Ile Pro Leu Gly Lys Leu Ser Gly
165 170 175
Arg His Ala Phe Val Glu Lys Leu Arg Glu Leu Ala Leu Asp Phe Thr
180 185 190
Glu Glu Asp Ile Lys Pro Phe Phe Ala Lys Phe Lys Ala Leu Ala Asp
195 200 205
Lys Lys
210

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

Met Ser Gln Gln Val Lys Asn Ala His Asn Leu Tyr Ile His Ala Ile
 1 5 10 15
 Gln Asp Gly Arg Val Ala Glu Ala Gln Ala Gln Ser Val Gly Asp Thr
 20 25 30
 Tyr Ile Gln His Ser Thr Gly Val Pro Asp Gly Lys Glu Gly Phe Ala
 35 40 45
 Ala Phe Phe Ala Asp Phe Phe Glu Arg His Pro Glu Arg Gln Ile Lys
 50 55 60
 Ile Val Arg Thr Ile Glu Asp Gly Asn Leu Val Phe Val His Val Pro
 65 70 75 80
 Ser Ile Ser Glu Trp Trp Arg Ser Ser Met Gly Asp Asp Gly Tyr Phe
 85 90 95
 Pro Cys Gly

(2) INFORMATION FOR SEQ ID NO:329:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

Met Glu Met Gln Thr Ser Ala Gln Leu Leu Thr Asn Lys Ile Phe Leu
 1 5 10 15
 Lys Asn Pro Leu Lys Ala Leu Val Glu Glu Lys Tyr Gly Ile Glu Tyr
 20 25 30
 Glu Glu Phe Thr Asn Pro Trp His Ala Ala Ile Ser Ser Phe Val Ala
 35 40 45
 Phe Phe Leu Arg Ser Leu Pro Pro Met Leu Ser Val Thr Ile Phe Pro
 50 55 60
 Ser Glu Tyr Arg Ile Pro Ala Thr Val Leu Ile Val Gly Val Ala Leu
 65 70 75 80
 Leu Leu Thr Gly Tyr Thr Ser Ala Arg Leu Gly Lys Asp Pro Thr Arg
 85 90 95
 Thr Ala Met Ile Arg Asn Leu Ala Ile Gly Leu Leu Thr Met Gly Val
 100 105 110
 Thr Phe Leu Leu Glu Gln Leu Phe Ser Ile
 115 120

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

Met Ala Phe Phe Leu Cys Pro His Phe Arg Ser Asn His Trp Lys Ile			
1	5	10	15
Leu Thr Val Ser Asp Thr Met Glu Glu Lys Arg Leu Glu Tyr Pro Met			
20	25	30	
Val Thr Phe Leu Gly Asn Pro Val Ser Phe Thr Gly Lys Gln Leu Gln			
35	40	45	
Val Gly Asp Lys Ala Leu Asp Phe Ser Leu Thr Thr Thr Asp Leu Ser			
50	55	60	
Lys Lys Ser Leu Ala Asp Phe Asp Gly Lys Lys Val Leu Ser Val			
65	70	75	80
Val Pro Ser Ile Asp Thr Gly Ile Cys Ser Thr Gln Thr Arg Arg Phe			
85	90	95	
Asn Glu Glu Leu Ala Gly Leu Asp Asn Thr Val Val Leu Thr Val Ser			
100	105	110	
Met Asp Leu Pro Phe Ala Gln Lys Arg Trp Cys Gly Ala Glu Gly Leu			
115	120	125	
Asp Asn Ala Ile Met Leu Ser Asp Tyr Phe Asp His Ser Phe Gly Arg			
130	135	140	
Asp Tyr Ala Leu Leu Ile Asn Glu Trp His Leu Leu Ala Arg Ala Val			
145	150	155	160
Phe Val Leu Asp Thr Asp Asn Thr Ile Arg Tyr Val Glu Tyr Val Asp			
165	170	175	
Asn Ile Asn Ser Glu Pro Asn Phe Glu Ala Ala Ile Ala Ala Lys			
180	185	190	
Ala Leu			

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

Met Gly Tyr Arg Pro Ser Thr Ala Asn Ala Ile Ile His Gln Val Arg
1 5 10 15
Glu Leu Leu Val Ser Arg Gly Tyr Thr Phe Tyr Asn Arg Lys Arg Leu
20 25 30
Met Val Val Pro Lys Ser Val Val Lys Glu Leu Leu Gly Met Glu Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:332:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

Met Gln Ala Val Glu His Phe Ile Lys Gln Phe Val Pro Glu His Tyr
1 5 10 15
Asp Leu Phe Leu Asp Leu Ser Arg Glu Thr Lys Thr Phe Ser Gly Lys
20 25 30
Val Thr Ile Thr Gly Gln Ala Gln Ser Asp Arg Ile Ser Leu His Gln
35 40 45
Lys Asp Leu Glu Ile Thr Ser Val Glu Val Ala Gly Gln Ala Arg Pro
50 55 60
Phe Thr Val Asp His Asp Asn Glu Ala Leu His Ile Glu Leu Ala Glu
65 70 75 80
Ala Gly Gln Val Glu Leu Val Leu Ala Phe Ser Gly Lys Ile Thr Asp
85 90 95
Asn Met Thr Gly Ile Tyr Pro Ser Tyr Tyr Val Asp Gly Val Lys
100 105 110
Lys Glu Val Leu Ser Thr Gln Phe Glu Ser His Phe Ala Arg Glu Ala
115 120 125

Phe Pro Cys Val Asp Glu Pro Glu Ala Lys Ala Thr Phe Asp Leu Ser
130 135 140
Leu Arg Phe Asp Gln Ala Glu Gly Glu Leu Ala Leu Ser Asn Met Pro
145 150 155 160
Glu Ile Asp Val Glu Asn Arg Lys Glu Thr Gly Ile Trp Lys Phe Glu
165 170 175
Thr Thr Pro Arg Met Ser Ser Tyr Leu Leu Ala Phe Val Ala Gly Asp
180 185 190
Leu Gln Gly Val Thr Ala Lys Thr Lys Asn Gly Thr Leu Val Gly Cys
195 200 205
Leu Leu Asn Gln Ser Thr Ser Thr Phe Lys Ser
210 215

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

Met Ser Gln Glu Phe Leu Ala Arg Ile Leu Glu Gln Lys Ala Arg Glu
1 5 10 15
Val Glu Gln Met Lys Leu Glu Gln Ile Gln Pro Leu Arg Gln Thr Tyr
20 25 30
Arg Leu Ala Glu Phe Leu Lys Asn His Gln Asp Arg Leu Gln Val Ile
35 40 45
Ala Glu Val Lys Lys Ala Ser Pro Ser Phe Gly Glu Ile Ser Ile Ser
50 55 60
Met Trp Ile Leu Cys Asn Arg Pro Arg Leu Met Lys Lys Thr Glu Gln
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

Met	Ser	Ser	Phe	Thr	Pro	Glu	Asp	Leu	Gly	Met	Glu	Gly	Tyr	Ala	Met
1					5					10					15
Glu	Asp	Ile	Arg	Gly	Gly	Asn	Ala	Gln	Glu	Asn	Ala	Glu	Ile	Leu	Leu
							20			25					30
Ser	Val	Leu	Lys	Asn	Glu	Ala	Ser	Pro	Phe	Leu	Glu	Thr	Thr	Val	Leu
							35			40					45
Asn	Ala	Gly	Leu	Gly	Phe	Tyr	Ala	Asn	Gly	Lys	Ile	Asp	Ser	Ile	Lys
							50			55					60
Glu	Gly	Val	Ala	Leu	Ala	Arg	Gln	Val	Ile	Ala	Arg	Gly	Lys	Ala	Leu
							65			70					80
Glu	Lys	Leu	Arg	Leu	Leu	Gln	Glu	Tyr	Gln	Lys					
							85			90					

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

Met	Ile	Tyr	Thr	Val	Thr	Leu	Asn	Pro	Ser	Ile	Asp	Tyr	Ile	Val	Arg
1						5				10					15
Leu	Asp	Gln	Val	Lys	Val	Gly	Ser	Val	Asn	Arg	Met	Asp	Ser	Asp	Asp
							20			25					30
Lys	Phe	Ala	Gly	Gly	Lys	Gly	Ile	Asn	Val	Ser	Arg	Val	Leu	Lys	Arg
							35			40					45
Leu	Asn	Ile	Ser	Asn	Thr	Ala	Thr	Gly	Phe	Ile	Gly	Gly	Phe	Thr	Gly
							50			55					60
Lys	Phe	Xaa	Xaa	Asp	Thr	Leu	Ala	Glu	Glu	Ile	Glu	Xaa	Arg	Phe	
							65			70					80
Val	Gln	Val	Ala	Glu	Asp	Thr	Arg	Ile	Asn	Val	Lys	Ile	Xaa	Ala	Asp
							85			90					95
Gln	Glu	Thr	Glu	Ile	Asn	Gly	Thr	Gly	Pro	Thr	Val	Glu	Pro	Val	Lys
							100			105					110

Leu Glu Glu Leu Lys Ala Ile Leu Ser Ser Leu Thr Ala Glu Asp Thr
115 120 125
Val Val Phe Ala Gly Ser Ser Ala Lys Asn Leu Gly Asn Val Ile Tyr
130 135 140
Lys Gly Phe Asn Leu Leu Asp Ala Pro Asp Trp Cys Ala Ser Gly Leu
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

Met Met Gln Val Tyr Phe Asp Gln Gly Ile Tyr Asn Lys Lys Ala Val
1 5 10 15
Phe Glu Val Tyr Phe Arg Gln Gln Pro Phe Lys Asn Gly Tyr Ala Val
20 25 30
Phe Ala Gly Leu Glu Arg Ile Val Asn Tyr Leu Glu Asp Leu Arg Phe
35 40 45
Ser Asp Ser Asp Ile Ala Tyr Leu Glu Ser Leu Gly Tyr His Gly Ala
50 55 60
Phe Leu Asp Tyr Leu Arg Asn Phe Lys Leu Glu Leu Thr Val Arg Ser
65 70 75 80
Ala Gln Glu Gly Asp Leu Val Phe Ala Asn Glu Pro Ile Val Gln Val
85 90 95
Glu Gly Pro Leu Ala Gln Cys Gln Leu Val Glu Thr Ala Leu Leu Asn
100 105 110
Ile Val Asn Tyr Gln Thr Leu Val Ala Thr Lys Ala Ala Pro Tyr Pro
115 120 125
Phe Gly Tyr Arg Lys
130

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

Met Lys Ile Ile Ile Gln Arg Val Lys Lys Ala Gln Val Ser Ile Glu
1 5 10 15
Gly Gln Ile Gln Gly Lys Ile Asn Gln Gly Leu Leu Leu Leu Val Gly
20 25 30
Val Gly Pro Glu Asp Gln Glu Glu Asp Leu Asp Tyr Ala Val Arg Lys
35 40 45
Leu Val Asn Met Arg Ile Phe Ser Asp Val Glu Gly Lys Met Asn Leu
50 55 60
Ser Val Lys Asp Ile Glu Gly Glu Ile Leu Ser Ile Leu Ser Leu Pro
65 70 75 80
Leu Cys Gly Tyr

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

Met Ile Lys Gly Thr Ile Lys Thr Val Ser Ile Met Ala Ala Thr Ser
1 5 10 15
Gly Phe Leu Leu Tyr Asn Glu Val Phe Phe Leu Thr Asn Gly Ala Ala
20 25 30
Gly Thr Lys Ser Ile Ser Phe Val Ile Arg Glu Leu Ala Val Ala Ser
35 40 45
Ser Arg Thr Gln Tyr Ala Arg Ala Asn Thr Ile Gly Val Ile Gln Ile
50 55 60
Leu Gly Gly Met Leu Ile Ile Val Cys Ile Asn Ile Leu Phe Arg Glu
65 70 75 80
Arg Lys Arg Leu Lys Gly Gly Lys
85

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

Met Gly Phe Gly Ile Pro Ala Ala Ile Gly Ala Lys Ile Ala Asn Pro
1 5 10 15
Asp Lys Glu Val Val Leu Phe Val Gly Asp Gly Gly Phe Gln Met Thr
20 25 30
Asn Gln Glu Leu Ala Ile Leu Asn Ile Tyr Lys Val Pro Ile Lys Val
35 40 45
Val Met Leu Asn Asn His Ser Leu Gly Met Val Arg Gln Trp Gln Glu
50 55 60
Ser Phe Tyr Glu Gly Arg Thr Ser Glu Ser Val Phe Asp Thr Leu Pro
65 70 75 80
Asp Phe Gln Leu Met Ala Gln Ala Tyr Gly Ile Lys Asn Tyr Lys Phe
85 90 95
Asp Asn Pro Glu Thr Leu Ala Gln Asp Leu Glu Ala Thr Thr Glu Asp
100 105 110
Val Pro Met Leu Ile Glu Val Asp Ile Ser Arg Lys Glu Gln Val Leu
115 120 125
Pro Met Val Pro Ala Gly Lys Ser Asn His Glu Met Leu Gly Val Lys
130 135 140
Phe His Ala
145

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

Met Trp Leu Pro Leu Asp Arg Asn Asn Lys Gly Gln Asn Ile Ala Gly
 1 5 10 15
 Ala Arg Gln Ala Ala Glu Gly Ile Phe Gly Val Asp Ala Ser Gln Leu
 20 25 30
 Thr Val Pro Gln Ala Ala Phe Leu Ala Gly Leu Pro Gln Ser Pro Ile
 35 40 45
 Thr Tyr Ser Pro Tyr Glu Asn Thr Gly Glu Leu Lys Asn
 50 55 60

(2) INFORMATION FOR SEQ ID NO:341:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

Met Tyr Leu Gly Asp Leu Met Glu Lys Ala Glu Cys Gly Gln Phe Ser
 1 5 10 15
 Ile Leu Ser Phe Leu Leu Gln Glu Ser Gln Thr Thr Val Lys Ala Val
 20 25 30
 Met Glu Glu Thr Gly Phe Ser Lys Ala Thr Leu Thr Lys Tyr Val Thr
 35 40 45
 Leu Leu Asn Asp Lys Ala Leu Asp Ser Gly Leu Glu Leu Thr Ile His
 50 55 60
 Ser Glu Asp Glu Asn Leu Arg Leu Ser Ile Gly Ala Ala Thr Lys Gly
 65 70 75 80
 Arg Asp Ile Pro Glu Leu Val Phe Trp Ile Val Leu Leu Asn Thr Arg
 85 90 95
 Phe Trp Phe Ile Phe Ser Thr Thr Asn Ser Phe
 100 105

(2) INFORMATION FOR SEQ ID NO:342:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

Met Lys Glu Ile Ile Glu Lys Leu Ala Lys Phe Glu Asn Leu Ser Gly
1 5 10 15
Val Glu Met Thr Asp Val Ile Glu Arg Ile Val Thr Gly Arg Val Thr
20 25 30
Glu Ala Gln Ile Ala Ser Leu Leu Leu Ala Lys Met Lys Gly Glu
35 40 45
Thr Pro Glu Glu Arg Thr Ala Ile Ala Gln Val Met Arg Gly His Ala
50 55 60
Gln His Ile Pro Thr Glu Ile His Asp Ala Met Asp Asn Cys Gly Thr
65 70 75 80
Gly Gly Asp Lys Ser Phe Ser Phe Asn Ile Ser Thr Thr Ala Ala Phe
85 90 95
Val Leu Ala Gly Gly Ile His Met Ala Lys His Gly Asn Arg Ser
100 105 110
Ile Ser Ser Lys Ser Gly Ser Ala Asp Ser Xaa Asn Leu Gly Asn Gln
115 120 125
Ser

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

Met Asn Val Gln Met Ser Ser Lys Thr Asn Ile Leu Arg Ala His Ala
1 5 10 15
Glu Met Gln Asn Ile Gln Arg Arg Ala Asn Glu Glu Arg Gln Asn Leu
20 25 30
Gln Arg Tyr Arg Ser Gln Asp Leu Ala Lys Ala Ile Leu Pro Ser Leu
35 40 45
Asp Asn Leu Glu Arg Ala Leu Ala Val Glu Gly Leu Thr Asp Asp Val
50 55 60

Lys Lys Gly Leu Gly Met Val Gln Glu Ser Leu Ile His Ala Leu Lys
 65 70 75 80
 Glu Glu Gly Ile Glu Glu Ile Ala Ala Asp Gly Glu Phe Asp His Asn
 85 90 95
 Tyr His Met Ala Ile Gln Thr Leu Pro Ala Asp Asp Asp His Pro Val
 100 105 110
 Asp Thr Ile Ala Gln Val Phe Gln Lys Gly Tyr Lys Leu His Asp Arg
 115 120 125
 Ile Leu Arg Pro Ala Met Val Val Val Tyr Asn
 130 135

(2) INFORMATION FOR SEQ ID NO:344:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

Met Ser Asn Lys Ser Tyr Ser Lys Phe Gln Glu Glu Val Ser Leu Lys
 1 5 10 15
 Tyr Gly Phe Ile Gly Leu Lys Leu Asp Lys Leu Ser Leu Thr Ala Glu
 20 25 30
 Val Ser Glu Glu Phe His Ser Glu Ile Leu Ser Gly Asn Phe Thr Leu
 35 40 45
 Tyr Asp Ile Ser Val
 50

(2) INFORMATION FOR SEQ ID NO:345:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

Met His Phe Asp Lys Ser Lys Phe Gly Ala Val Phe Ser Ala Pro Gly
1 5 10 15
Leu Tyr Glu Val Glu Val Ile Asn Asn Ala Ser Phe Gly Gln Asn Ala
20 25 30
Gln Tyr Glu Val Ile Gln Ser Arg Lys Leu Gly Thr Phe Ala Glu Leu
35 40 45
Ile Glu Met Ala Lys Ile Lys
50 55

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Met Ile Gln Ala Val Phe Glu Arg Ala Glu Asp Gly Glu Leu Arg Ser
1 5 10 15
Ala Glu Ile Thr Gly His Ala Glu Ser Gly Glu Tyr Gly Leu Asp Val
20 25 30
Val Cys Ala Ser Val Ser Thr Leu Ala Ile Asn Phe Ile Asn Ser Ile
35 40 45
Glu Lys Phe Ala Gly Tyr Glu Pro Ile Leu Glu Leu Asn Glu Asp Glu
50 55 60
Gly Gly Tyr Leu Met Val Glu Ile Pro Lys Asp Leu Pro Ser His Gln
65 70 75 80
Arg Glu Met Thr Gln Leu Phe Phe Glu Ser Phe Phe Leu Gly Met Ala
85 90 95
Asn Leu Ser Glu Asn Ser Ser Glu Phe Val Gln Thr Arg Val Ile Thr
100 105 110
Glu Asn

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

Met	Thr	Ala	Ile	Ser	Met	Lys	Trp	Leu	Asn	Asp	Tyr	Ile	Trp	Pro	Ala
1					5				10				15		
Glu	Ser	Glu	Phe	Thr	Pro	Asp	Met	Thr	Thr	Asn	Ala	Val	Lys	Glu	Ala
					20				25			30			
Leu	Thr	Glu	Met	Leu	Gln	Ser	Gly	Thr	Thr	Thr	Phe	Asn	Asp	Met	Tyr
					35				40			45			
Asn	Pro	Asn	Gly	Val	Asp	Ile	Gln	Gln	Ile	Tyr	Gln	Val	Val	Lys	Thr
					50				55			60			
Ser	Lys	Met	Arg	Cys	Tyr	Phe	Ser	Pro	Thr	Leu	Phe	Ser	Ser	Glu	Thr
					65				70			75			80
Glu	Thr	Thr	Ala	Glu	Thr	Ile	Ser	Arg	Thr	Arg	Ser	Ile	Ile	Asp	Glu
					85				90			95			
Ile	Leu	Lys	Tyr	Lys	Asn	Pro	Lys	Phe	Gln	Gly	Leu	Trp			
					100				105						

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

Met	Val	Arg	Glu	Ser	Ala	Glu	Ser	Ala	Gly	Phe	Phe	Leu	Glu	Thr	His
1					5				10			15			
Met	Val	Gln	Gly	Glu	Trp	Asn	Thr	Cys	Val	Phe	Lys	Lys	Thr	Lys	Asp
					20				25			30			
Ile	Ser	Gly	Val	Ile	Gly	Gly									
					35										

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

Met Thr Val Asp Arg Glu Gly Phe Glu Ala Ala Met Lys Glu Gln Gln
1 5 10 15
Glu Arg Ala Arg Ala Ser Ala Val Lys Gly Gly Ser Met Gly Met Gln
20 25 30
Asn Gly Asn Ser Ser Lys His His Cys Arg Lys Cys Leu Gln Leu Gln
35 40 45
Cys

(2) INFORMATION FOR SEQ ID NO:350:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

Met Lys Ala Gln Leu Val Pro Ser Arg Ser Lys Tyr Leu Ile Asn Asp
1 5 10 15
Asn Thr Val Val Leu Phe Phe Gly Thr Arg Thr Asp Tyr Thr Arg Lys
20 25 30
Tyr Asp Leu Asp Leu Val Arg Glu Val Ala Gly Asp Gln Ile Ala Arg
35 40 45
Arg Val Val Leu Leu Ser Asp Gln Ala Phe Gly Leu Glu Asn Val Lys
50 55 60
Glu Val Ala Leu Gly Cys Gly Gly Val Leu Asn Asp Ile Tyr Arg Val
65 70 75 80
Phe Pro Tyr Ile Val Tyr Ala Gln Leu Phe Ala Leu Leu Thr Ser Leu
85 90 95
Lys Val Glu Asn Lys Pro Asp Thr Pro Ser Pro Thr Gly Thr Val Asn
100 105 110

Arg Val Val Gln Gly Val Ile Ile His Glu Tyr Gln Lys
115 120 125

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

Met Ala Val Asn Asn Glu Ile Gly Ser Ile Gln Xaa Ile Glu Ala Ile
1 5 10 15
Ser Glu Phe Leu Ala Asp Lys Pro Thr Ile Ser Phe His Val Asp Ala
20 25 30
Val Gln Ala Leu Ala Lys Ile Pro Thr Glu Lys Tyr Leu Thr Glu Arg
35 40 45
Val Asp Cys Ala Thr Phe Ser Ser His Lys Phe His Gly Val Arg Gly
50 55 60
Val Gly Phe Val Tyr Ile Lys Ser Gly Lys Lys Ile Thr Pro Leu Leu
65 70 75 80
Thr Gly Gly Gln Glu Arg Asp Tyr Arg Ser Thr Thr Glu Asn Val
85 90 95
Ala Gly Ile Ala Ala Thr Ala Lys Ala Leu Arg Leu Ser Met Glu Lys
100 105 110
Leu Asp Ile Phe Arg Ser Lys Thr Gly Gln Met Lys Ala Val Ile His
115 120 125
Gln Ala Leu Leu Asn Tyr Pro Asp Ile Phe Val Phe Ser Asp Glu Glu
130 135 140
Asp Phe Ala Pro His Ile Leu Thr Phe Gly Ile Lys Gly Val Arg Gly
145 150 155 160
Glu Val Ile Val His Ala Phe Glu Asp Tyr Asp Ile Phe Ile Ser Thr
165 170 175
Thr Ser Ala Cys Ser Ser Lys Ala Gly Lys Pro Ala Gly Thr Leu Ile
180 185 190
Ala Met Gly Val Asp Lys Asp Lys Ala Lys Ser Ala Val Arg Leu Ser
195 200 205
Leu Asp Leu Glu Asn Asp Met Ser Gln Val Glu Gln Phe Leu Thr Lys
210 215 220

Leu Lys Leu Ile Tyr Asn Gln Thr Arg Lys Val Arg
225 230 235

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

Met Leu Val Thr Gly Ala Ile Leu Gly Val Asn Val His Ile Phe Ser
1 5 10 15
Pro Lys Glu Leu Phe Pro Glu Lys Glu Ile Val Glu Leu Ala Glu Gly
20 25 30
Phe Ala Lys Glu Ser Gly Ala His Val Leu Ile Thr Glu Asp Ala Asp
35 40 45
Glu Ala Val Lys Asp Ala Asp Val Leu Tyr Thr Asp Val Trp Val Ser
50 55 60
Met Gly Glu Glu Asp Lys Phe Ala Glu Arg Val Ala Leu Leu Lys Pro
65 70 75 80
Tyr Gln Val Asn Met Asp Leu Val Lys Lys Ala Gly Asn Glu Asn Leu
85 90 95
Ile Phe Leu His Cys Leu Pro Ala Phe His Asp Thr His Thr Val Tyr
100 105 110
Gly Lys Asp Val Ala Glu Lys Phe Gly Val Glu Glu Met Glu Val Thr
115 120 125
Asp Glu Val Phe Arg Ser Lys Tyr Ala Arg His Phe Asp Gln Ala Glu
130 135 140
Asn Arg Met His Thr Ile Lys Ala Val Met Ala Ala Thr Leu Gly Asn
145 150 155 160
Leu Tyr Ile Pro Lys Val
165

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

Met	Arg	Leu	Glu	Gln	Asp	Cys	Pro	Val	Phe	Leu	Lys	Ile	Lys	Glu	Lys
1										10					15
Asp	Met	Ala	Ser	Lys	Met	Leu	His	Thr	Cys	Leu	Arg	Val	Glu	Asn	Leu
					20				25					30	
Glu	Lys	Ser	Ile	Ala	Phe	Tyr	Gln	Asp	Ala	Phe	Gly	Phe	Lys	Glu	Leu
					35				40				45		
Arg	Arg	Arg	Asp	Phe	Pro	Asp	His	Ala	Phe	Thr	Ile	Val	Tyr	Leu	Gly
					50				55			60			
Leu	Glu	Gly	Asp	Asp	Tyr	Glu	Leu	Glu	Leu	Thr	Tyr	Asn	Tyr	Asp	His
					65				70		75		80		
Gly	Pro	Tyr	Val	Val	Gly	Asp	Gly	Phe	Ala	His	Ile	Ala	Ser	Thr	
					85				90			95			
Pro	Asp	Leu	Glu	Ala	Leu	His	Gln	Glu	His	Ser	Thr	Lys	Gly	Tyr	Gl
					100				105			110			
Val	Thr	Glu	Pro	Asn	Gly	Leu	Pro	Gly	Thr	Ala	Pro	Asn	Tyr	Tyr	Phe
					115				120			125			
Val	Lys	Asp	Pro	Asp	Gly	Tyr	Lys	Val	Glu	Val	Ile	Arg	Glu	Lys	
					130				135			140			

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

Met	Asp	His	Thr	Ile	Phe	Cys	Val	Gly	Tyr	Arg	Val	Met	Gln	Lys	Asp
1										10					15
Leu	Glu	Gly	Thr	Leu	Asp	Ala	Glu	Lys	Leu	Lys	Ala	Ala	Gly	Val	Pro
					20				25			30			
Phe	Gly	Pro	Leu	Phe	Gly	Lys	Ile	Lys	Asn	Gly	Gln	Asp	Leu	Val	Leu
					35				40			45			

Glu Asp Gly Thr Glu Ile Lys Ala Ala Asp Tyr Ile Ser Ala Pro Arg
 50 55 60
 Pro Gly Lys Ile Ile Thr Ile Leu Gly Asp Thr Arg Lys Thr Asp Ala
 65 70 75 80
 Ser Val Arg Leu Ala Val Asn Ala Asp Val Leu Val His Glu Ser Thr
 85 90 95
 Tyr Gly Lys Gly Asp Glu Lys Ile Ala Arg Asn His Gly His Ser Thr
 100 105 110
 Asn Met Gln Ala Ala Gln Val Ala Val Glu Ala Gly Ala Lys Arg Leu
 115 120 125
 Leu Leu Asn His Ile Ser Ala Arg Phe Leu Ser Lys Asp Ile Ser Lys
 130 135 140
 Leu Lys Lys Asp Ala Ala Thr Ile Phe Glu Asn Val His Val Val Lys
 145 150 155 160
 Asp Leu Glu Lys Met Glu Ile Tyr Gln Ser Gln Lys Gly
 165 170

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

Met Ile Gln Pro Ala Ser Leu Glu Glu Leu Ala Ser Leu Val Glu Lys
 1 5 10 15
 Ala Gly Lys Lys Val Phe Leu Phe Val Ala Asp Trp Cys Gly Asp Cys
 20 25 30
 Arg Tyr Ile Tyr Pro Ala Leu Pro Glu Ile Glu Glu Thr Asn Pro Glu
 35 40 45
 Phe Thr Phe Ile Arg Met Asp Arg Asp Gln Tyr Met Asp Leu Ala Lys
 50 55 60
 Leu Trp Asp Val Tyr Gly Ile Pro Ser Leu Val Val Leu Glu Lys Asp
 65 70 75 80
 Lys Glu Ile Gly Arg Phe Val Asn Arg Asp Arg Lys Ser Lys Glu Gln
 85 90 95
 Ile Asn Asp Phe Leu Ala Gly Leu Lys
 100 105

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

Met Arg Leu Gly Leu Leu Gln Val Leu Arg Leu Pro Lys Ala Phe Gln
1 5 10 15
Leu Ile Phe Ile Gln Asp Lys Gly His Gly Asp Val Ser Ser Phe Thr
20 25 30
Ala Ser Cys Val Thr Gly Pro Trp Ala Phe Lys Leu Val Gly Lys Gln
35 40 45
Gly Asn Ile His
50

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

Met Lys Thr Arg Lys Ile Pro Leu Arg Lys Ser Val Val Ser Asn Glu
1 5 10 15
Val Ile Asp Lys Arg Asp Leu Leu Arg Ile Val Lys Asn Lys Glu Gly
20 25 30
Gln Val Phe Ile Asp Pro Thr Gly Lys Ala Asn Gly Arg Gly Ala Tyr
35 40 45
Ile Lys Leu Asp Asn Ala Glu Ala Leu Glu Ala Lys Lys Lys Lys Val
50 55 60
Phe Asn Arg Ser Phe Ser Met Glu Val Glu Glu Ser Phe Tyr Asp Glu
65 70 75 80

Leu Ile Ala Tyr Val Asp His Lys Val Lys Arg Arg Glu Leu Gly Leu
85 90 95
Glu

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

```

Met Arg Val Ala Tyr Phe Lys Val His His Pro Ile Tyr Tyr Tyr Cys
   1             5                 10                15
Ala Tyr Phe Ser Ile Arg Ala Lys Ala Phe Asp Ile Lys Thr Met Gly
   20            25                 30
Ala Gly Leu Glu Val Ile Lys Arg Arg Met Glu Glu Ile Ser Glu Lys
   35            40                 45
Arg Lys Asn Asn Glu Ala Ser Asn Val Glu Ile Asp Leu Tyr Thr Thr
   50            55                 60
Leu Glu Ile Val Asn Glu Met Trp Glu Arg Gly Phe Lys Phe Gly Lys
   65            70                 75                 80
Leu Asp Leu Tyr Cys Ser Gln Thr Thr Glu Phe Leu Ile Asp Gly Asp
   85            90                 95
Thr Leu Ile Pro Pro Phe Val Ala Met Asp Gly Leu Gly Glu Asn Val
   100           105                110
Ala Lys Gln Leu Val Arg Ala Arg Glu Glu Gly Glu Phe Leu Ser Lys
   115           120                125
Thr Glu Leu Arg Lys Arg Gly Gly Leu Ser Ser Thr Leu Val Glu Lys
   130           135                140
Met Asp Glu Met Gly Ile Leu Gly Asn Met Pro Glu Ile Thr Ser
   145           150                155

```

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

Met Ser Ser Lys Ile Ser Ile Gly Gln Leu Ile Thr Phe Asn Thr Leu
1 5 10 15
Leu Ser Tyr Phe Thr Thr Pro Met Glu Asn Ile Ile Asn Leu Gln Thr
20 25 30
Lys Leu Gln Ser Ala Lys Val Ala Asn Asn Arg Leu Asn Glu Val Tyr
35 40 45
Leu Val Glu Ser Glu Phe Gln Val Gln Glu Asn Pro Val His Ser His
50 55 60
Phe Leu Met Gly Asp Ile Glu Phe Asp Asp Leu Ser Tyr Lys Tyr Gly
65 70 75 80
Phe Gly Arg Asp Thr Leu Thr Asp Ile Asn Leu Thr Ile Lys Gln Gly
85 90 95
Asp Lys Val Ser Leu Val Gly Val Ser Gly Ser Gly Lys Thr Thr Leu
100 105 110
Ala Lys Met Ile Val Asn Phe Phe Glu Pro Tyr Lys Gly His Ile Ser
115 120 125
Ile Asn His Gln Asp Ile Lys Asn Ile Asp Lys Lys Ser Leu Ala Pro
130 135 140
Ser Tyr
145

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

Met Arg Gln Ala Pro Ala Leu Ala Gln Ala Asn Ile Glu Arg Val Val
1 5 10 15
Val His Lys Ile Ser Lys Val Trp Glu Phe His Phe Arg Ile Phe
20 25 30

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

Met Gln Thr Gly Trp Gln Tyr Leu Gly Asn Lys Trp Tyr Tyr Leu Arg
1 5 10 15
Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Gln Glu Gly Thr Thr Trp
20 25 30
Tyr Tyr Leu Asp Gln Pro Asn Gly Asp Met Lys Thr Gly Trp Gln Asn
35 40 45
Leu Gly Asn Lys Trp Tyr Tyr Leu Arg Ser Ser Gly Ala Met Ala Thr
50 55 60
Gly Trp Tyr Gln Glu Gly Thr Thr Trp Tyr Tyr Leu Asp Gln Pro Asn
65 70 75 80
Gly Asp Met Lys Thr Gly Trp Gln Asn Leu Gly Asn Lys Trp Tyr Tyr
85 90 95
Leu Arg Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Gln Asp Gly Ser
100 105 110
Thr Trp Tyr Tyr Leu Asn Ala Val Met Glu Ile
115 120

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

Met Lys Trp Gly Ser Arg Ile Leu Leu Gly Leu Thr Pro Lys Ser Leu
1 5 10 15

Arg Tyr Arg Ile Trp Lys Lys Ala Glu Lys Glu Met Thr Lys Tyr Asp
 20 25 30
 Leu Ala Asp Cys Asp Gly Ile Thr Glu Leu Cys Ser Gly Pro Gly Tyr
 35 40 45
 Met Arg Asn Lys Tyr Pro Ile Thr Ser Phe Glu Asp Asn Leu Phe Leu
 50 55 60
 Pro Phe Glu Gly Thr Glu Met Pro Ile Pro Ile Gly Tyr Asp Val Tyr
 65 70 75 80
 Leu Arg Thr Ala Phe Gly Asp Tyr Met Thr Pro Pro Pro Ala Asp Lys
 85 90 95
 Gln Val Pro His Gln Asp Ala Val Ile Ala Asp Met Asp Lys Ser Tyr
 100 105 110
 Thr Glu Tyr Lys Gly Glu Tyr Gly Gly
 115 120

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

Met Phe Pro Asp Ser Ile Asp Thr Met His Gln Ala Asn Glu Phe Ile
 1 5 10 15
 Ala Leu Asp Asp Leu Phe Arg Ala Ala Ala Ile Tyr Ala Glu Ala Ile
 20 25 30
 Tyr Glu Leu Ile Lys
 35

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

Met Asp Glu Leu Gln Lys Arg Asn Leu Leu Gly Phe Val Phe Gln Asp
1 5 10 15
Phe Gln Leu Phe Pro His Leu Ser Val Leu Glu Asn Leu Thr Leu Ser
20 25 30
Pro Val Lys Thr Met Gly Met Lys Gln Glu Glu Ala Glu Lys Lys Ala
35 40 45
Ser Gly Leu Leu Glu Gln Leu Gly Leu Gly His Ala Glu Ser Tyr
50 55 60
Pro Phe Ser Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Leu Ala Arg
65 70 75 80
Ala Met Met Ile Asp Pro Glu Ile Ile Gly Tyr Asp Glu Pro Thr Ser
85 90 95
Ala Leu Asp Pro Glu Leu Arg Leu Glu Val Glu Lys Leu Ile Leu Gln
100 105 110
Asn Arg Glu Leu Gly Met Thr His Ile Val Val Thr His Asp Leu Gln
115 120 125
Phe Gly
130

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

Met Tyr Gly Ala Asn Ser Glu Arg Leu Lys Glu Ser Leu Arg Ile Ser
1 5 10 15
Leu Ser Pro Gln Asn Thr Val Glu Asp Leu Gln Thr Leu Ala Lys Thr
20 25 30
Leu Lys Glu Ile Ile Gly Gly
35

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

```

Met Ile Ala Arg Ser Tyr Gln Glu Met Asp Asp Leu Asp Thr Ala Tyr
 1           5           10          15
Glu His Tyr Gln Glu Leu Thr Gly Asp Leu Lys Asp Asn Pro Glu Phe
 20          25          30
Leu Glu His Tyr Ile Tyr Leu Leu Arg
 35          40

```

(2) INFORMATION FOR SEQ ID NO:367:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

```

Met Lys His Phe Asp Thr Ile Val Ile Gly Gly Gly Pro Ala Gly Met
 1           5           10          15
Met Ala Thr Ile Ser Ser Ser Phe Tyr Gly Gln Lys Thr Leu Leu Ile
 20          25          30
Glu Lys Asn Arg Lys Leu Gly Lys Lys Leu Ala Gly Thr Gly Gly Gly
 35          40          45
Arg Cys Asn Val Thr Asn Asn Gly Ser Leu Asp Asn Leu Leu Ala Gly
 50          55          60
Ile Pro Gly Asn Gly Arg Phe Leu Tyr Ser Val Phe Ser Gln Phe Asp
 65          70          75          80
Asn His Asp Ile Ile Asn Phe Phe Thr Glu Asn Gly Val Lys Leu Lys
 85          90          95
Val Glu Asp His Gly Arg Val Phe Pro Ala Ser Asp Lys Ser Arg Thr
100         105         110
Ile Ile Glu Ala Leu Glu Lys Lys Ile Thr Glu Leu Gly Gly Gln Val
115         120         125

```

Ala Thr Pro Asn Arg Asn Arg Phe Cys
 130 135

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

Met	Thr	Leu	Ala	Lys	Asp	Ile	Ala	Ser	His	Leu	Leu	Lys	Ile	Gln	Ala
1															
														15	
Val	Tyr	Leu	Lys	Pro	Glu	Glu	Pro	Phe	Thr	Trp	Ala	Ser	Gly	Ile	Lys
														30	
Ser	Pro	Ile	Tyr	Thr	Asp	Asn	Arg	Val	Thr	Leu	Ala	Tyr	Pro	Glu	Thr
														45	
Arg	Thr	Leu	Ile	Glu	Asn	Gly	Phe	Val	Glu	Ala	Ile	Lys	Glu	Ala	Phe
														50	
50														55	
Pro	Glu	Val	Glu	Val	Ile	Ala	Gly	Thr	Ala	Thr	Ala	Gly	Ile	Pro	His
65														75	
Gly	Ala	Ile	Ile	Ala	Asp	Lys	Met	Asp	Leu	Pro	Phe	Ala	Tyr	Ile	Pro
														85	
														90	
														95	

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

Met	Val	Lys	Val	Leu	Ala	Ala	Cys	Gly	Asn	Gly	Met	Gly	Ser	Ser	Met
1															
														15	
Val	Ile	Lys	Met	Lys	Val	Glu	Asn	Ala	Leu	Arg	Lys	Leu	Asn	Gln	Thr
														20	
														25	
														30	

Asp Phe Thr Val Asn Ser Cys Ser Val Gly Glu Ala Lys Gly Leu Ala			
35	40	45	
Val Gly Tyr Asp Ile Val Ile Ala Ser Leu His Leu Ile Gln Glu Leu			
50	55	60	
Glu Gly Arg Thr Asn Gly Lys Leu Ile Gly Leu Asp Asn Leu Met Asp			
65	70	75	80
Asp Lys Glu Ile Thr Glu Lys Leu Ser Gln Ala Ile Gln			
85	90		

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

Met Ser Met Phe Leu Asp Thr Ala Lys Ile Lys Val Lys Ala Gly Asn			
1	5	10	15
Gly Gly Asp Gly Met Val Ala Phe Arg Arg Glu Lys Tyr Val Pro Asn			
20	25	30	
Gly Gly Pro Trp Gly Gly Asp Gly Gly Arg Gly Gly Asn Val Val Phe			
35	40	45	
Val Val Asp Glu Gly Leu Arg Thr Leu Met Asp Phe Arg Tyr Asn Arg			
50	55	60	
His Phe Lys Ala Asp Ser Gly Glu Lys Gly Met Thr Lys Gly Met His			
65	70	75	80
Gly Arg Gly Ala Glu Asp Leu Arg Val Arg Val Pro Gln Gly Thr Thr			
85	90	95	
Val Arg Asp Ala Glu Thr Gly Lys Val Leu Thr Asp Leu Ile Glu His			
100	105	110	
Gly Gln Glu Phe Ile Val Ala His Gly Gly Pro Trp Trp Thr Trp Lys			
115	120	125	
Tyr Ser Phe Arg Asp Thr Lys Lys Ser Cys Thr Gly Asn Leu			
130	135	140	

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

Met	Met	Lys	Gly	Glu	Met	Thr	Phe	Lys	Gln	Val	His	Tyr	Lys	Tyr	Gly
1				5					10				15		
Tyr	Gly	Arg	Asp	Val	Leu	Ser	Asp	Ile	Asn	Leu	Thr	Val	Pro	Gln	Gly
				20					25				30		
Ser	Lys	Val	Ala	Phe	Val	Gly	Ile	Ser	Gly	Ser	Gly	Lys	Thr	Thr	Leu
				35					40				45		
Ala	Lys	Met	Met	Val	Asn	Phe	Tyr	Asp	Pro	Ser	Gln	Glu	Ile	Ser	
				50				55				60			
Leu	Gly	Gly	Val	Asn	Leu	Asn	Gln	Ile	Asp	Lys	Lys	Ala	Leu	Arg	Gln
				65				70			75			80	
Tyr	Ile	Ile	Tyr	Leu	Pro	Pro	Gln	Pro	Tyr	Val	Phe	Asn	Gly	Thr	Ile
					85				90				95		
Leu	Glu	Asn	Leu	Leu	Gly	Ala	Lys	Gly	Gly	Asp	Asp	Thr	Gly	Lys	
				100				105				110			
Ile	Ser	Leu	Thr	Gly	Arg	Ser	Glu	Phe	Gly	Ser	Glu	Ile	Pro	Lys	Arg
				115				120				125			
Asn	Ile	Ser	Lys	Pro	Pro	Cys	His	Leu	Glu	Ile	Tyr	Gln	Thr	Glu	Leu
				130				135				140			
Thr	Ser	Asp	Gly	Ala	Gly	Ile	Ser	Gly	Gly	Gln	Arg	Gln	Arg	Ile	Ala
				145				150			155			160	
Leu	Ala	Arg	Ala	Leu	Leu	Thr	Asp	Ala	Pro	Val	Leu	Ile	Leu	Asp	Glu
					165				170			175			
Ala	Thr	Asn	Ser	Leu	Asp	Ile	Leu	Thr	Lys	Lys	Arg	Ile	Val	His	Tyr
					180				185			190			
Leu	Met	Ala	Leu	Asp	Lys	Thr	Phe	Asp	Phe	His	Cys	Ser	Pro	Leu	Asp
					195				200			205			
Tyr	Cys														
	210														

(2) INFORMATION FOR SEQ ID NO:372:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

Met Ala Arg Phe Ile Glu Ile Asp Ala Lys Glu His Asp Arg Val Thr
1 5 10 15
Ser Gln Ile Ser His Phe Pro His Ile Leu Ala Ser Ser Leu Met Glu
20 25 30
Gln Thr Ala Val Tyr Ala Gln Glu His Glu Asn Gly Lys Ala Leu Cys
35 40 45
Gly Arg Trp Phe Ser Arg Tyr Asp Pro Asn Cys Gly Lys Arg Ala Arg
50 55 60
Asn Val Asp Leu His Ser Leu Val Gln
65 70

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

Met Ala His Gln Gly Gln Asp Ile Tyr Asp Phe Pro Arg Ala Met Ile
1 5 10 15
Lys Glu Asp Asn Leu Glu Phe Ser Phe Ser Gly Leu Lys Ser Ala Phe
20 25 30
Ile Asn Leu His His Asn Ala Glu Gln Lys Gly Glu Ser Leu Ser Thr
35 40 45
Glu Asp Leu Cys Ala Ser Phe Gln Ala Ala Val Leu Asp Ile Leu Met
50 55 60
Ala Lys Thr Lys Lys Ala Leu Glu Lys Tyr Pro Val Lys Thr Leu Val
65 70 75 80
Val Ala Gly Gly Val Ala Ala Asn Lys Gly Leu Arg Glu Arg Leu Ala
85 90 95
Ala Glu Val Thr Asp Val Lys Val Ile Ile Pro Pro Leu Arg Leu Cys
100 105 110
Gly Asp Asn Ala Gly Met Ile Ala Tyr Ala Ser Val Ser Glu Trp Asn
115 120 125

Lys Glu Asn Phe Ala Asn Leu Asp Leu Asn Ala Lys Pro Ser Leu Ala
130 135 140
Phe Asp Thr Met Glu
145

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

Met Lys Arg Ser Leu Asp Ser Arg Val Asp Tyr Ser Leu Leu Leu Pro
1 5 10 15
Val Phe Phe Leu Leu Val Ile Gly Val Val Ala Ile Tyr Ile Ala Val
20 25 30
Ser His Asp Tyr Pro Asn Asn Ile Leu Pro Ile Leu Gly Gln Gln Val
35 40 45
Ala Trp Ile Ala Leu Gly Leu Val Ile Gly Phe Val Val Met Leu Phe
50 55 60
Asn Thr Glu Phe Leu Trp Lys Val Thr Pro Phe Leu Tyr Ile Phe Arg
65 70 75 80
Leu Gly Thr Tyr Asp Leu Ala Asp Cys Ile Leu
85 90

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

Met Pro Asp Asp Ile Ile Asp Ser Phe Trp Tyr Ile Ile Asp His Phe
1 5 10 15

Leu Lys Asn Val Phe Glu Leu Glu Glu Leu Glu Phe Gln Leu Leu
20 25 30
Asn Asn Gln Gly Lys Ile Thr Phe His Phe Ser Ser Gln His Leu Pro
35 40 45
Thr Ala Ile Asp Phe Asp Phe Asn His Pro Phe Asp Pro Arg Tyr Pro
50 55 60
Pro Arg Val Leu Val Leu Asp Met Asp Gly Arg Glu Thr Ile Leu Leu
65 70 75 80
Pro Glu Glu Asn Asp Leu Phe
85

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

Met Gly Lys Lys Asp Ala Ser Ala Met His Glu Met Arg Ala Ser Phe
1 5 10 15
Ile Gln Gly Ser Ile Glu Ala Gly His Thr Ala Glu Lys Ser Glu Gln
20 25 30
Val Phe Asp Val Met Glu Lys Phe Ala Gly Tyr Gly Phe Asn Arg Ser
35 40 45
His Ala Tyr Ala Tyr Ser Ala Leu Ala Phe Gln Leu Ala Tyr Phe Lys
50 55 60
Thr His Tyr Pro Ala Ile Phe Tyr Gln Val Met Leu Asn Tyr Ser Asn
65 70 75 80
Ser Asp Tyr Leu Ile Asp Ala Leu Glu Ala Gly Phe Glu Val Ala Ser
85 90 95
Leu Ser Ile Asn Thr Ile Pro Tyr His Asp Lys Ile Ala Asn Lys Ser
100 105 110
Ile Tyr Ile Gly Leu Lys Ser Ile Lys Gly Leu Gln Gln Gly Leu Gly
115 120 125
Ala Leu Asp Tyr
130

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

Met Asp Lys Lys Gln Asn Leu Thr Ser Phe Gln Glu Leu Thr Thr Thr
1 5 10 15
Glu Leu Asn Gln Ile Thr Gly Gly Glu Trp Trp Glu Glu Leu Leu His
20 25 30
Glu Thr Ile Leu Ser Lys Phe Lys Ile Thr Lys Ala Leu Glu Leu Pro
35 40 45
Ile Gln Leu
50

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

Met His Glu Met Phe Thr Ala Ile Ala Glu Ser Asp Met Lys Lys Ala
1 5 10 15
Ala Ala Ile Gln Arg Lys Phe Ile Pro Lys Val Asn Ala Leu Phe Ser
20 25 30
Tyr Pro Ser Pro Ala Pro Val Lys Ala Ile Leu Asn Tyr Met Gly Phe
35 40 45
Glu Ala Gly Pro Thr Arg Leu Pro Leu Val Pro Ala Pro Glu Glu Asp
50 55 60
Val Lys Arg Ile Ile Lys Val Val Val Asp Gly Asp Tyr Glu Ala Thr
65 70 75 80
Lys Ala Thr Val Thr Gly Val Leu Arg Pro Asp Tyr
85 90

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

Met Leu Asn Glu Phe Pro Ile Phe Asp Tyr Glu Asp Ile Gln Leu Ile
1 5 10 15
Pro Asn Lys Cys Val Ile Lys Ser Arg Ala Glu Ala Asp Thr Ser Val
20 25 30
Thr Leu Gly Asn His Thr Phe Lys Leu Pro Val Val Pro Ala Asn Met
35 40 45
Gln Thr Ile Leu Asp Glu Asn Val Ala Glu Gln Leu Ala Lys Gly Gly
50 55 60
Tyr Leu Tyr Thr Tyr Ala Pro Phe
65 70

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

Met Asp Ile Lys Leu Lys Asp Phe Glu Gly Pro Leu Asp Leu Leu
1 5 10 15
His Leu Val Ser Lys Tyr Gln Met Asp Ile Tyr Asp Val Pro Ile Thr
20 25 30
Glu Val Ile Glu Gln Tyr Leu Ala Tyr Val Ser Thr Leu Gln Ala Met
35 40 45
Arg Leu Glu Val Thr Gly Glu Tyr Met Val Met Ala Ser Gln Leu Met
50 55 60

Leu Ile Lys Ser Arg Lys Leu Leu Pro Lys Val Ala Glu Val Thr Asp
 65 70 75 80
 Leu Gly Asp Asp Leu Glu Gln Asp Leu Leu Ser Gln Ile Glu Glu Tyr
 85 90 95
 Arg Lys Phe Lys Leu Leu Gly Glu His Leu Glu Ala Lys His Gln Glu
 100 105 110
 Thr Gly Pro Val Leu Phe Gln Ser Ala Asp Arg Val Asp Leu Arg Arg
 115 120 125
 Cys Gly Ala Cys Ala
 130

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

Met Gln Ser Thr Glu Lys Lys Pro Leu Thr Ala Phe Thr Xaa Ile Ser
 1 5 10 15
 Thr Ile Ile Leu Leu Leu Leu Thr Val Leu Xaa Ile Phe Pro Phe Tyr
 20 25 30
 Trp Ile Leu Thr Gly Ala Phe Lys Ser Gln Pro Asp Thr Ile Val Ile
 35 40 45
 Pro Pro Gln Trp Phe Pro Lys Met Pro Thr Met Glu Asn Phe Gln Gln
 50 55 60
 Leu Met Val Gln Asn Pro Ala Leu Gin Trp Met Trp Asn Ser Val Phe
 65 70 75 80
 Ile Ser Leu Val Thr Met Phe Leu Val Cys Ala Thr Ser Ser Leu Ala
 85 90 95
 Gly Tyr Val Leu Ala Xaa Lys Arg Phe Tyr Gly Xaa Arg Ile Tyr Cys
 100 105 110

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

Met Leu Phe Met Arg Asp Ser Leu Asp Ser Ile Val Glu Pro Val Leu
1 5 10 15
Asp Glu Met Gly Arg Phe Tyr Asp Trp Thr Glu Glu Glu Lys Ala Thr
20 25 30
Tyr Arg Ala Asp Val Lys Ala Ala Leu Ala Gln Asn Asp Leu Ala Glu
35 40 45
Leu Lys Asn
50

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

Met Lys Ile Lys Val Val Thr Val Gly Lys Leu Lys Glu Lys Tyr Leu
1 5 10 15
Lys Asp Gly Ile Ala Glu Tyr Ser Lys Arg Ile Ser Arg Phe Ala Lys
20 25 30
Phe Glu Met Ile Glu Leu Ser Asp Glu Lys Thr Pro Asp Lys Ala Ser
35 40 45
Glu Ser Glu Asn Gln Lys Ile Leu Glu Ile Glu Gly Gln Arg Ile Leu
50 55 60
Ser Lys Ile Ala Asp Arg Asp Phe Val Ile Val Leu Ala Ile Glu Gly
65 70 75 80
Lys Thr Phe Phe Ser Glu Glu Phe Ser Lys Gln Leu Glu Glu Thr Ser
85 90 95
Ile Lys Gly Xaa Ser Thr Leu Thr Phe Ile Ile Gly Gly Ser Leu Gly
100 105 110
Leu Ser Ser Ser Val Lys Asn Arg Ala Asn Leu Ser Val Ser Phe Gly
115 120 125

Arg Leu Thr Leu Pro His Gln Leu Met Arg Leu Val Leu Val Glu Gln
130 135 140
Ile Tyr Arg Ala Phe Thr Ile Gln Gln Gly Phe Pro Tyr His Lys
145 150 155

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

Met Gly Ile Leu Ala Trp Cys Asp Leu Val Leu Tyr Arg Leu Trp Asp
1 5 10 15
Ser Phe Met Asp Leu Gly Leu Phe Ile Asn Asp Ala Trp Val Arg Lys
20 25 30
Lys Lys Thr Leu Asn Lys Glu Arg Lys Lys Ala Gly Lys Ala Ala Leu
35 40 45
Pro Glu Asn Arg Trp Ile Gln Leu Leu Gly Met Val Val Thr Phe His
50 55 60
Val Val Met Leu Ser Phe Leu Ile Phe Ser Gly Phe Leu Asn Asn Leu
65 70 75 80
Trp Phe Lys Lys

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

Met Val Met Ala Glu Asp Gln Ala Val Arg Gln Asn Arg Leu Ala Ile
1 5 10 15

Leu Ser Gln Leu Thr Lys Lys Ala Ala Lys Phe Ala Cys Phe Asn Gln
20 25 30
Ile Asn Thr Lys
35

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

Met Gly Ala Gln Pro Val Gln Asp Thr Glu Thr Ser Ser Ala Leu Ile
1 5 10 15
Ser Ser His Tyr Leu Asp Glu Gln Asp Leu Ser Glu Lys Leu Lys Ser
20 25 30
Glu Leu Gln Trp Phe Glu Leu Glu Asn Lys Leu Leu Asn Leu Trp Glu
35 40 45
His

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

Met Asp Glu Val Thr Ile Phe Gly Ile Asn Tyr Phe Lys Glu His Tyr
1 5 10 15
Pro Glu Lys Leu Ala Glu Arg Phe Lys Gln Met Lys Ile Glu Glu Glu
20 25 30
Ala Pro Val Ile Ile Met Asp Met Thr Arg Ala Leu Gly Phe Arg Asp
35 40 45

Asp Tyr Asp Arg Phe Tyr Ser Leu Phe Arg Glu Gly Ser Pro
50 55 60

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

Met Lys Val Ile Asn Gln Thr Leu Leu Glu Lys Val Ile Ile Glu Arg
1 5 10 15
Ser Arg Ser Ser His Lys Gly Asp Tyr Gly Xaa Leu Leu Leu Leu Gly
20 25 30
Gly Thr Tyr Pro Tyr Gly Val Xaa Ser Ser Trp Leu Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

Met Asn Trp Ile Leu Leu Gln Gly Leu Ile Cys Gln Arg Asp Ala Ser
1 5 10 15
Tyr Asp Met Lys Gln Asp Asp Leu Asp Lys Val Ala Asp Tyr Leu Phe
20 25 30
Lys Thr Glu Glu Trp Thr Met Tyr Glu Leu Ile Leu Phe Gly Asn Leu
35 40 45
Tyr Ser Phe Tyr Asp Val Asp Tyr Val Thr Arg Ile Gly Arg Glu Val
50 55 60
Met Glu Arg Glu Glu Phe Tyr Gln Glu Ile Ser Arg His Lys Arg Leu
65 70 75 80

Val	Leu	Ile	Leu	Ala	Leu	Asn	Cys	Tyr	Gln	His	Cys	Leu	Glu	His	Ser
85									90						95
Ser	Phe	Tyr	Asn	Ala	Asn	Tyr	Phe	Glu	Ala	Tyr	Thr	Glu	Lys	Ile	Ile
100									105						110
Asp	Lys	Gly	Ile	Lys	Leu	Tyr	Glu	Arg	Asn	Val	Phe	His	Tyr	Leu	Lys
115									120						125
Gly	Phe	Ala	Leu	Tyr	Gln	Lys	Gly	Gln	Cys	Lys	Glu	Gly	Cys	Lys	Gln
130									135						140
Met	Gln	Glu	Thr	Met	His	Ile	Phe	Asp	Val	Leu	Gly	Leu	Pro	Glu	Gln
145									150						160
Val	Ser	Leu	Leu	Ser	Gly	Thr	Leu	Arg	Lys	Ile	Cys	Gln	Lys	Leu	Ile
165									170						175
Phe	Pro	Asn	Lys	Gly	Lys	Asn	Lys	Lys	Leu	Leu	Ser	Val	Leu	Ile	Gln
180									185						190

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

Met	Ser	Thr	Val	Leu	Ser	Trp	Thr	Ala	Tyr	Lys	Thr	Gln	Arg	Leu	Glu
1															
	5							10							15
Met	Ser	Ile	Leu	Leu	His	Met	Ile	Val	Asn	Gly	Ile	Ala	Phe	Cys	Leu
	20								25						30
Leu	Ala	Leu	Val	Val	Ile	Met	Ser	Arg	Thr	Leu	Gly	Ile	Ser	Val	
	35								40						45

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

Met Arg Glu Asn Asp Leu Leu Leu Ile Thr Ala Asp His Gly Asn Asp
1 5 10 15
Pro Thr Tyr Ala Gly Thr Asp His Thr Arg Glu Tyr Ile Pro Leu Leu
20 25 30
Ala Tyr Ser Pro Ala Phe Lys Gly Asn Gly Leu Ile Pro Val Gly His
35 40 45
Phe Ala Asp Ile Ser Ala Thr Val Ala Asp Asn Phe Gly Val Glu Thr
50 55 60
Ala Met Ile Gly Glu Ser Phe Leu Asp Lys Leu Val
65 70 75

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

Met Lys Lys Ile Phe Leu Thr Leu Leu Thr Val Ser Leu Leu Gly Gly
1 5 10 15
Ala Ser Thr Ala Val Ala Gln Asp Phe Thr Ile Ala Ala Lys His Ala
20 25 30
Ile Ala Val Glu Ala Asn Thr Gly Lys Ile Leu Tyr Glu Lys Asp Ala
35 40 45
Thr Pro Pro Val Glu Ile Ala Ser Ile Thr Lys Leu Ile Thr Val Tyr
50 55 60
Leu Val Tyr Glu Ala Leu Glu Asn Gly Ser Ile Thr Leu Ser Thr Pro
65 70 75 80
Val Asp Ile Ser Asp Tyr Pro Tyr Gln Leu Thr Thr Asn Ser Glu Ala
85 90 95
Ser Asn Ile Pro Met Glu Ala Arg Asn Tyr Thr Val Glu Glu Leu Leu
100 105 110
Glu Ala Thr Leu Val Ser Ser Ala Asn Ser Ala Ala Ile Ala Leu Ala
115 120 125
Glu Lys Ile Ala Gly Ser Glu Lys Asp Phe Val Xaa Met Met Arg Ala
130 135 140

Lys Leu Leu Glu Trp Gly Ile Arg Ile His Cys Cys Gln Tyr Asp Arg
145 150 155 160
Ser

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

Met Ser Asn Ala Met Glu Gly Val Leu Tyr Phe Leu Lys Pro Asp Phe
1 5 10 15
Ser Lys Leu Thr Ser Ala Asp Leu Leu Tyr Ala Leu Gly Gln Ser Phe
20 25 30
Phe Ala Leu Ser Leu Gly Val Thr Asp Met Leu Thr Tyr Ala Ser Tyr
35 40 45
Leu Asp Lys Lys Thr Asn Leu Val Gln Ser Gly Ile Ser Ile Val Thr
50 55 60
Met Asn Ile Ser Ile Val His His Gly Arg Ser Ser His Phe Pro Ser
65 70 75 80
His Val Ser Leu Gln Tyr Pro Leu
85

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

Met Lys Val Ala Lys Pro Phe Trp Ala Ile Val Lys Leu Lys Ser Val
1 5 10 15

Gln His Ala Ser Met Leu Glu Asn Pro Lys Glu Met Asp Gly Leu Met
20 25 30
Lys Gln Val Glu Asn Leu Ala Leu Glu Asn Gln Gly Tyr Gln Val Glu
35 40 45
Lys Glu Asn Lys Ala Phe Glu Gln Ile Lys Asp Ser Val Ala Thr Phe
50 55 60
Gln Thr Phe Leu Thr Ile Phe Leu Tyr Gly Cys
65 70 75

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

Met Asp Ala Glu Val Ser Lys Asn Leu Arg Leu Ile Leu Glu Arg Lys
1 5 10 15
Gly Met Thr Ile Leu Thr Gly Thr Lys Leu Gln Glu Ile Ile Glu Glu
20 25 30
Asn Gly Gln Leu Arg Ile Lys Val Glu Gly Lys Asp Asn Ile Ile Ala
35 40 45
Ser Lys Ala Leu Leu Ser Ile Gly Arg Met Pro Asp Leu Glu Gly Ile
50 55 60
Gly Glu Val Glu Phe Glu Leu Asp Arg Gly Cys Ile Lys Val Asn Glu
65 70 75 80
Tyr Met Glu Thr Ser Val Pro Arg Ile Tyr Ala Thr Arg
85 90

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

Met Lys Asn Ser Ile Met Asp Thr Lys Phe Asp Arg Arg Ile Leu Leu
1 5 10 15
Leu Asn Lys Ile Ile Ile Val Phe Ile Val Leu Met Thr Leu Leu Pro
20 25 30
Leu Leu Tyr Ile Val Val Ala Ser Phe Met Asp Pro Lys Val Leu Val
35 40 45
Ser Arg Gly Ile Ser Phe Asn Pro Ala Asp Trp Thr Val Glu Gly Tyr
50 55 60
Gln Arg Val Ile Gln
65

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

Met Val Ile Pro Glu Ala Gly Tyr Leu Tyr Ala Phe His Tyr Pro Asn
1 5 10 15
Leu Lys Gly Lys Gly Lys Glu Ala Val Gln Val Ile Tyr Asn Leu Asn
20 25 30
Leu Ala Ser Ala Lys Val Ile Gln Leu Tyr Arg Ser Leu Gly Leu Asp
35 40 45
Gly Lys Ile Gly Ile Ile Leu Asn Leu Thr Pro Ala Tyr Pro Arg Ser
50 55 60
Asn Ser Pro Glu Asp Leu Glu Ala Ser Arg Phe Thr Asp Asp Phe Phe
65 70 75 80
Asn Lys Val Phe Leu Glu Ser Ser Cys
85

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

Met	Thr	Arg	Ile	Ala	Ser	Val	Ser	Val	Ile	Arg	Asn	Ala	Ala	Phe	Ile
1					5				10						15
Ala	Ile	Ala	Leu	Ser	Phe	Leu	Gly	Lys	Phe	Thr	Ala	Leu	Ile	Ser	Thr
					20				25						30
Ile	Pro	Asn	Ala	Val	Leu	Gly	Gly	Met	Ser	Ile	Leu	Leu	Tyr	Gly	Val
					35				40						45
Ile	Ala	Ser	Asn	Gly	Leu	Lys	Val	Leu	Ile	Lys	Glu	Arg	Val	Asp	Phe
					50				55						60
Ala	Gln	Met	Arg	Asn	Leu	Ile	Ile	Ala	Ser	Ala	Met	Leu	Val	Leu	Gly
					65				70						80
Leu	Gly	Arg	Ser	Tyr	Pro										
					85										

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

Met	Ser	Leu	Arg	Glu	Lys	Ser	Met	Ser	Glu	Tyr	Lys	Leu	Ser	Glu	Asn
1						5				10					15
Asn	Trp	Thr	Arg	Val	Ala	Val	Phe	Ala	Gly	Gly	Asn	Arg	Gly	His	Tyr
							20			25					30
Arg	Thr	Asp	Phe	Asp	Ala	Phe	Val	Gly	Val	Asp	Arg	Gly	Ser	Leu	Trp
							35			40					45
Val	Leu	Glu	Glu	Asp	Leu	Pro	Leu	Ala	Leu	Ala	Val	Gly	Asp	Phe	Asp
							50			55					60
Ser	Val	Thr	Glu	Glu	Glu	Arg	Gln	Val	Ile	Gln	Lys	Arg	Ala	Gln	Tyr
							65			70					80
Phe	Val	Gln	Ala	Arg	Pro	Glu	Lys	Asp	Asp	Thr	Asp	Leu	Glu	Leu	Ala
								85			90				95

Leu Leu Thr Ile Phe Glu Gln Asn Pro Gln Ala Glu Val Thr Ile Phe
100 105 110
Gly Ala Leu Gly Gly Arg Ile Asp His Met Leu Ala Asn Val Leu Ser
115 120 125
Thr

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

Met Val Leu Gln Arg Asn Glu Ile Asn Glu Lys Asp Thr Trp Asp Leu
1 5 10 15
Ser Thr Ile Tyr Pro Thr Asp Gln Ala Trp Glu Glu Ala Leu Lys Asp
20 25 30
Leu Thr Glu Gln Leu Glu Thr Val Ala Gln Tyr Glu Gly His Leu Leu
35 40 45
Asp Ser Ala Asp Asn Leu Leu Val Asn His
50 55

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

Met Ile Tyr Gly Ala Ile Ile Asp Ala Lys Thr Ala Glu Asn Ala Ala
1 5 10 15
Gly Met Thr Ala Met Gln Thr Ala Thr Asp Asn Ala Lys Lys Val Ile
20 25 30

Asn Asp Leu Thr Ile Gln Tyr Asn Arg Ala Gln Thr Gly Gly Tyr Tyr
35 40 45
Thr Arg Asn Tyr Arg Asn Arg Ser Ser Ala
50 55

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

Met Thr Asp Gly Tyr Glu His Tyr Lys Lys Ile Met Glu Asn Pro Pro
1 5 10 15
Lys Asn Leu Ile Phe Pro Gly Ile Val Ser Pro Glu Arg Met Arg Glu
20 25 30
Ile Val Cys Ser Asn Gly Ser Phe Leu Val Ala
35 40

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

Met Ser Lys Gln Lys Lys Phe Glu Glu Asn Leu Ala Glu Leu Glu Thr
1 5 10 15
Ile Val Gln Ser Leu Glu Asn Gly Glu Ile Ala Leu Glu Asp Ala Ile
20 25 30
Thr Ala Phe Gln Lys Gly Met Val Leu Ser Lys Glu Leu Gln Ala Thr
35 40 45
Leu Asp Lys Ala Glu Lys Thr Leu Val Lys Val Met Gln Glu Asp Gly
50 55 60

Thr Glu Ser Asp Phe Glu
65 70

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

Met Phe Ala Ala Val Thr Ala Gly Tyr Gln Ala Ala Leu Met Val Pro
1 5 10 15
Thr Glu Ile Leu Ala Glu Gln His Phe Glu Ser Leu Gln Asn Leu Phe
20 25 30
Pro Asn Leu Lys Leu Ala Leu Leu Thr Gly Ser Leu Lys Ala Ala Glu
35 40 45
Lys Arg Glu Val Leu Glu Thr Ile Ala Lys Gly Glu Ala Asp Leu Ile
50 55 60
Ile Gly Thr His Ala Leu Ile Gln Asp Gly Val Glu Tyr Ala Arg Leu
65 70 75 80
Gly Leu Ile Ile Ile Asp Glu Gln His Arg Phe Gly Val Gly Gln Arg
85 90 95
Arg Ile Leu Arg Glu Lys Gly Asp Asn Pro Asp Val Leu Met Met Thr
100 105 110
Ala Thr Pro Ile Pro Arg Thr Leu Ala Ile Thr Ala Phe Gly Asp Met
115 120 125
Asp Val Ser Ile Ile Asp Gln Met Pro Ala Gly Arg Lys Pro Tyr Cys
130 135 140
Asp Ala Leu Asp Gln Thr
145 150

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

Met Asn Arg Glu Ala Leu Arg Leu Tyr Leu Val Thr Asn Arg Tyr Gln
1 5 10 15
Asp Ser Val Glu Ser Phe Leu Ala Lys Val Glu Thr Ala Cys Arg Ser
20 25 30
Gly Val Thr Ile Val Gln Leu Arg Glu Lys Asn Leu Thr Thr Asn Gln
35 40 45
Tyr Tyr Gln Leu Ala Lys Gln Val Lys Glu Ile Thr Asp Ala Tyr Gln
50 55 60
Val Pro Leu Ile Ile Asp Asp Arg Leu Asp Val Cys Leu Ala Val Asp
65 70 75 80
Ala Ala Gly Leu His Ile Gly Asp Asp Glu Leu Pro Val Ser Val Ala
85 90 95
Arg Gln Val Leu Gly Pro Glu Lys Ile Pro Arg Cys His Arg
100 105 110

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

Met Gln Gly Ser His Phe His Leu Pro Ile Tyr Arg Met Thr Ser Gln
1 5 10 15
Ala Leu Leu Asp Glu Thr Lys Lys Val Ala Ile Pro Val Leu Ala Thr
20 25 30
Thr Gln Ser Lys Asp Ser Val Asp Tyr Arg Glu Leu Pro Ser Ile Glu
35 40 45
Asn Phe Val Leu Val Met Gly Asn Glu Gly Gln Gly Ile Ser Pro Leu
50 55 60
Met Ala Glu Ser Ala Asp Gln Leu Val His Ile Ser Met Lys Gly Gln
65 70 75 80
Ala Glu Ser Leu Asn Val Ala Val Ala Gly Ile Leu Ile Phe His
85 90 95
Leu Ser

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

Met	Thr	Lys	Thr	Ala	Phe	Leu	Phe	Ala	Gly	Gln	Gly	Ala	Gln	Tyr	Leu
1				5				10				15			
Arg	Met	Gly	Arg	Asp	Phe	Tyr	Asp	Gln	Tyr	Pro	Ile	Val	Lys	Glu	Thr
					20				25				30		
Ile	Asp	Arg	Ala	Ser	Gln	Val	Leu	Gly	Tyr	Asp	Leu	Arg	Tyr	Leu	Ile
				35				40			45				
Asp	Thr	Glu	Glu	Asp	Lys	Leu	Asn	Gln	Thr	Arg	Tyr	Thr	Gln	Pro	Ala
				50			55			60					
Ile	Leu	Ala	Thr	Ser	Val	Ala	Ile	Tyr	Arg	Leu	Leu	Gln	Glu	Lys	Gly
				65			70			75			80		
Tyr	His	Pro	Asp	Met	Val	Ala	Gly	Leu	Ser	Leu	Gly	Glu	Tyr	Ser	Ala
				85				90			95				
Leu	Val	Ala	Ser	Gly	Ala	Leu	Asp	Phe	Glu	Asp	Ala	Val	Ala	Leu	Val
				100				105			110				
Ala	Lys	Arg	Gly	Ala	Tyr	Met	Glu	Glu	Ala	Ala	Pro	Ala	Asp	Ser	Gly
				115				120			125				
Lys	Met	Val	Ala	Val	Leu	His	Thr	Pro							
				130				135							

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

Met Tyr Gln Phe Ser Gly Gln Thr Lys Val Xaa Glu Val Leu Ala Phe
1 5 10 15
Arg Asp Lys Pro Pro Tyr Gly Gly Ser Ser Ala Met Pro Leu Arg Cys
20 25 30
Leu

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

Met Thr Lys Glu Thr Gly Met Glu Gln Thr Phe Phe Ile Ile Lys Pro
1 5 10 15
Asp Gly Val Lys Arg Gly Leu Val Gly Glu Val Leu Lys Arg Ile Glu
20 25 30
Gln Arg Gly Phe Thr Ile Glu Lys Leu Glu Phe Arg Ser Gln Val Phe
35 40 45
Arg Arg Val Asp
50

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

Met Thr Ser Gly Pro Val Leu Val Gly Val Ile Ser Gly Pro Lys Val
1 5 10 15

Ile	Glu	Thr	Trp	Arg	Thr	Met	Met	Gly	Ala	Thr	Arg	Pro	Glu	Glu	Ala
20						25							30		
Leu	Pro	Gly	Thr	Ile	Arg	Gly	Asp	Phe	Ala	Lys	Ala	Ala	Gly	Glu	Asn
35						40							45		
Glu	Ile	Ile	Gln	Asn	Val	Val	His	Gly	Ser	Asp	Ser	Glu	Lys	Asn	Gln
50						55							60		
Leu	Ser	Arg	Glu	Ile	Ala	Pro	Leu	Val	Leu	Arg	Val	Asp	Trp	Leu	Asn
65						70						75			80
Gln	Leu	Asp	Lys	Ser	Ser	Phe	Glu								
						85									

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

Met	Gly	Leu	Lys	Asp	Asn	Ala	Gly	Leu	Val	Lys	Glu	Tyr	Ala	Leu	Val
1						5			10				15		
Asp	Ala	Val	Glu	Tyr	Gln	Asn	Val	Ile	Val	Ala	Thr	Thr	Val	Glu	Glu
							20				25		30		
Met	Leu	Ser	Lys	Tyr	Ala	Asn	Lys	Asn	Asp	Leu	Glu	Ile	Asp	Asn	Ala
						35			40			45			
Thr	Thr	Glu	Ser	Ile	Lys	Gly	Val	Val	Ala	Asp	Leu	Lys	Ser	Ala	Val
						50			55			60			
Ile	Lys	Gly	Asp	Thr	Val	Tyr	Phe	Phe	Lys	Val	Asp	Gly	Lys	Ile	Tyr
65						70			75			80			
Lys	Val	Lys	Ala	Ser	Val	Ser	Asp	Asp	Leu	Pro	Tyr	Leu	Glu	Asn	Gly
						85			90			95			
Lys	Thr	Phe	Glu	Gly	Gln	Val	Xaa	Lys	Asp	Asn	Tyr	Leu	Lys	Thr	Phe
						100			105			110			
Lys	Val	Gln													
						115									

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

Met Ile Ser Gly Ser Glu Ile Arg Asp Ile Val Thr Ser Asp Ile Pro
1 5 10 15
Leu Ala Asp Lys Thr Glu Thr Leu Val Arg Phe Ala Asn Asn Ala Gly
20 25 30
Gly Leu Asp Asn Ile Thr Val Ala Leu Val Ser Met Asn Glu Glu Asp
35 40 45
Glu Glu
50

(2) INFORMATION FOR SEQ ID NO:413:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

Met Pro Asp Asn Leu Ala Leu Arg Met Arg Pro Lys Thr Ile Asp Gln
1 5 10 15
Val Ile Gly Gln Glu Xaa Leu Val Gly Pro Gly Lys Ile Ile Arg Arg
20 25 30
Met Val Glu Ala Asn Arg Leu Ser Ser Met Ile Leu Tyr Gly Pro Pro
35 40 45
Gly Ile Gly Lys Thr Ser Ile Ala Ser Ala Ile Ala Gly Thr Thr Lys
50 55 60
Tyr Ala Phe Arg Thr Phe Asn Ala Thr Val Asp Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:414:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

Met Pro Glu Glu Leu Ala Tyr Leu Val Gln His Leu Asp Asn Ala Gln
1 5 10 15
Glu Gln Val Val Leu Gly Asn Thr Tyr His Thr Gly Asn His Cys Phe
20 25 30
Ser

(2) INFORMATION FOR SEQ ID NO:415:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 45 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

Met Val Phe Trp Glu Gly Leu Val Pro Thr Pro Asp Val Ile Asp Ala
1 5 10 15
Gly His Val Thr Gly Phe Leu Tyr Thr Val His Ser Ser Ser Thr Gly
20 25 30
Leu Ile Val Leu Gln Ile Lys Lys Asp Leu Leu Lys Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:416:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 143 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

Met Thr Asp Arg Tyr Asp Ser Ser Leu Gly Ile Tyr Lys Val Pro Trp
1 5 10 15
Cys Val Ser Gln Gln Gln Thr Val Thr Glu Ile Met Asp Thr Tyr Cys
20 25 30
Asp Trp Gly Val Lys Tyr Pro Leu Val Tyr Leu Glu Asp Pro Phe Ser
35 40 45
Asp Glu Asp Leu Asp Ser Trp Arg Lys Phe Gln Leu Ile Lys Pro Leu
50 55 60
Lys Leu Gln Val Phe Gly Asp Asp Phe Tyr Ala Thr Asn Leu Glu Arg
65 70 75 80
Ile Ser Gln Phe Lys Asp Cys Ala Asp Gly Ile Val Ile Lys Pro Asn
85 90 95
Gln Val Gly Ser Val Ser Lys Thr Leu Glu Val Met Glu Tyr Ala Glu
100 105 110
Lys Ser Gly Ile Ser Met Ala Phe Ser Gln Arg Thr Ala Glu Thr Glu
115 120 125
Asn Asn Ile Ile Ser His Leu Ala Met Ser Val Ile Leu Leu Ile
130 135 140

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

Met Lys Lys Ile Ser Lys Gln Glu Leu Val Asn Thr Arg Phe Ser Arg
1 5 10 15
Leu Phe Ala His Phe Gly Gln Glu Lys Asp Gly Ser Phe Leu Ala Gln
20 25 30
Arg Tyr Gln Phe Tyr Leu Ala Gln Gln Gly Gln Thr Leu Ser Gly Ala
35 40 45
His Asp Leu Leu Asp Ser Leu Ile Glu Arg Asp Tyr Asn Leu Tyr Ala
50 55 60
Ala Thr Asn Gly Ile Thr Ala Ile Gln Thr Gly Arg Leu Ala Gln Ser
65 70 75 80

Gly Leu Ala Pro Tyr Phe Asn Gln Val	Phe Ile Ser Glu Gln	Leu Gln
85	90	95
Thr Gln Lys Pro Asp Ala Leu Phe	Tyr Glu Lys Ile Gly Gln	Gln Ile
100	105	110
Ala Gly Phe Ser Lys Glu Lys Thr		
115	120	

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

Met His Arg Lys Thr Val Ile Asp Xaa Arg Thr	Leu Gly Glu Arg Tyr		
1	5	10	15
Thr Phe Thr Xaa Pro Ile Lys Glu	Leu Lys Thr Arg Asn Val Ala Glu		
20	25	30	
Val Ala Asp Leu Leu Ala Xaa Val Glu Ser	Tyr Gln Glu Gln Asp Tyr		
35	40	45	
Tyr Val Val Gly Tyr Val Ser Tyr Glu Ala Ala	Pro Ala Phe Glu Glu		
50	55	60	
Lys Leu Ala Val His Lys Val Pro Leu Leu	Gly Glu Tyr Leu Leu Tyr		
65	70	75	80
Phe Thr Val His Asp Arg Val Glu Thr Ser	Pro Ile Pro Leu Thr Tyr		
85	90	95	
Glu Asp Ile Asp Leu Pro Ser Asn Trp Gln	Gly Xaa Asn Val Cys Thr		
100	105	110	
Glu Leu			

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

Met Glu Arg Ile Glu Val Arg Ser Arg Ser Gly Ser Ala His Leu Gly
1 5 10 15
His Val Phe Thr Asp Gly Pro Arg Glu Leu Gly Gly Leu Arg Tyr Cys
20 25 30
Ile Asn Ser Ala Ser Leu Arg Phe Val Ala Lys Asp Glu Met Glu Lys
35 40 45
Ala Gly Tyr Gly Tyr Leu Leu Pro Tyr Leu Asn Lys
50 55 60

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

Met Glu Trp Ile Arg Leu Ile Gly Ile Ala Ile Ile Val Val Gly Phe
1 5 10 15
Ile Leu Lys Phe Asp Thr Ile Ala Thr Val Val Leu Ala Gly Leu Val
20 25 30
Thr Ala Leu Val Ser Gly Val Ser Leu Val Glu Phe Leu Glu Ile Leu
35 40 45
Gly Lys Glu Phe Ser Asn Gln Arg Val Leu Thr Ile Phe Met Val Thr
50 55 60
Leu Pro Leu Val Gly Leu Ser Glu Thr Phe Gly Leu Asn Asn Asp Gln
65 70 75 80
Ser Ile

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

Met Leu Leu Ile Phe Ala Val Ile Gly Val Leu Val Ala Leu Ile Ala
1 5 10 15
Gln Phe Tyr Ser Ala Lys Ala Ala Val Gly Phe Ala Lys Glu Leu Thr
20 25 30
Asn Asp Leu Tyr Arg His Ile Leu Ser Leu Pro Lys Asp Ser Arg Asp
35 40 45
Arg Leu Thr Thr Ser Ser Leu Val Thr Arg Leu Thr Ser Asp Thr Tyr
50 55 60
Gln Ile Gln Thr Gly Ile Asn Gln Phe Leu Arg Leu Phe Leu Arg Ala
65 70 75 80
Pro Ile Ile Val Phe Gly Ala Ile Phe Met Ala Tyr Arg Ile Ser Ala
85 90 95
Glu Leu Thr Phe Trp Phe Leu Val Met Val Ala Ile Leu Thr Ile Val
100 105 110
Ile Val Arg Val Ile Ser Ile Gly Gln Ser Ser Leu Gln
115 120 125

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

Met Pro Ile Glu Gln Val Gln Lys Leu Leu Gly His Ser Lys Ile Asp
1 5 10 15
Thr Thr Leu Ala Tyr Ala Met Val Asn Gln Asn Asn Val Lys His Ser
20 25 30
His Gln Lys Phe Ile Ser
35

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

Met	Lys	Pro	Cys	Trp	Lys	Lys	Cys	Phe	Pro	Glu	Glu	Val	Ser	Ser	Glu
1					5				10				15		
Gly	Glu	Val	Thr	Leu	Ile	Glu	Ile	Pro	Val	Ser	Asp	Lys	Ile	Ala	Gly
					20				25				30		
Lys	Gln	Val	His	Glu	Leu	Asn	Leu	Pro	His	Asn	Val	Leu	Ile	Thr	Thr
					35				40			45			
Gln	Val	His	Asn	Gly	Lys	Ser	Gln	Thr	Val	Asn	Gly	Ser	Thr	Arg	Met
					50				55		60				
Tyr	Leu	Gly	Asp	Met	Ile	His	Leu	Val	Ile	Pro	Lys	Ser	Glu	Ile	Gly
					65				70		75		80		
Lys	Val	Lys	Asp	Leu	Leu	Leu									
					85										

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

Met	Asn	Glu	Gly	Val	Glu	Asn	Phe	Arg	Ala	Lys	Leu	Ala	Ser	Leu	Gly
1					5				10			15			
Ala	Lys	Asn	Ile	Gly	Ile	Tyr	Val	Gly	Val	Tyr	Phe	Met	Glu	Gly	
					20				25			30			
Ser	Ile	Asp	Thr	Gly	Lys	Phe	Thr	Ser	Val	Trp	Ile	Pro	Ser	Tyr	Gly
					35				40			45			
Ser	Asp	Ser	Gly	Phe	Leu	Glu	Ser	Ser	Pro	Lys	Thr	Asp	Leu	Asp	Tyr
					50				55		60				

Asp Ile His Gln Tyr Thr Ser Lys Gly Lys Leu Pro Ala Leu Thr Thr
65 70 75 80
Ile

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

Met Val Ser Lys Tyr Leu Leu Leu Ala Val Ile Phe Ser Gly Leu Val
1 5 10 15
Thr Trp Ile Leu Arg Met Ile Ser Phe Ile Leu Val Lys Tyr Lys Gly
20 25 30
Leu Pro Ala Ile Val Glu Arg Phe Leu Lys Phe Leu Pro Val Ser Ile
35 40 45
Ile Phe Ala Leu Ile Leu Ser Ser Val Val Thr Gly Lys Val Gly Ser
50 55 60
Leu Pro Gln Ile Lys Trp Leu Asp Phe Leu Ala Val Phe Pro Thr Ala
65 70 75 80
Trp Val Ala Phe Arg Tyr Arg Asn Leu Leu Gly Thr Val Leu Phe Gly
85 90 95
Val Val Leu Ile Ala Ile Leu Arg Leu Val Ser
100 105

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

Met Glu Asp Xaa Glu Thr Gln Arg Val Val Met Gln Tyr Arg Ala Pro
 1 5 10 15
 Glu Asn Asn Arg Trp Ser Gly Tyr Ala Phe Pro Gly Gly His Val Glu
 20 25 30
 Asn Asp Glu Ala Phe Ala Glu Ser Val Ile Arg Glu Ile Tyr Glu Glu
 35 40 45
 Thr Gly Leu Thr Ile Gln Asn Pro Gln Leu Val Gly Ile Lys Asn Trp
 50 55 60
 Pro Leu Asp Thr Gly Gly Arg Tyr Ile Val Ile Cys Tyr Lys Ala Thr
 65 70 75 80
 Glu Phe Ser Gly Thr Leu Gln Ser Ser Glu Glu Gly Glu Val Ser Trp
 85 90 95
 Val Gln Lys Asp Gln Ile Pro Asn Leu Asn Leu Ala Tyr Asp Met Leu
 100 105 110
 Pro Leu Met Glu Met Met Glu Ala Pro Asp Lys Ser Glu Phe Phe Tyr
 115 120 125
 Pro Arg Arg Thr Glu Asp Asp Trp Glu Lys Lys Ile Phe
 130 135 140

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

Met Thr Ile Glu Leu Leu Thr Pro Phe Thr Lys Val Glu Leu Glu Pro
 1 5 10 15
 Glu Ile Lys Glu Lys Lys Arg Lys Gln Val Gly Ile Leu Gly Gly Asn
 20 25 30
 Phe Asn Pro Val His Asn Ala His Leu Ile Val Ala Asp Gln Val Arg
 35 40 45
 Gln Gln Leu Gly Leu Asp Gln Val Leu Leu Met Pro Glu Tyr Gln Pro
 50 55 60
 Pro His Val
 65

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

Met	Lys	Lys	Leu	Val	Phe	Val	Cys	Leu	Gly	Asn	Ile	Cys	Arg	Ser	Pro
1															15
Met	Ala	Glu	Phe	Val	Met	Lys	Ser	Met	Thr	Asp	Asn	Tyr	Glu	Ile	Gln
	20								25					30	
Ser	Arg	Ala	Thr	Ser	Ser	Trp	Glu	His	Gly	Asn	Pro	Ile	His	Lys	Gly
	35						40						45		
Thr	Gln	Gly	Ile	Phe	Gln	Glu	Tyr	Glu	Ile	Pro	Tyr	Asp	Lys	Asn	Lys
	50					55				60					
Thr	Ser	Leu	Gln	Ile	Ser	Lys	Glu	Asp	Phe	Glu	Ala	Phe	Asp	Tyr	Ile
	65					70				75			80		
Ile	Gly	Met	Asp	Ala	Ser	Asn	Val	Pro	Thr	Tyr	Val	Arg	Cys	Val	Gln
							85			90			95		

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

Met	Val	Lys	Tyr	Gly	Val	Val	Gly	Ala	Gly	Tyr	Phe	Gly	Ala	Glu	Leu
1															15
Ala	Arg	Tyr	Met	Gln	Lys	Asn	Asp	Gly	Ala	Xaa	Ile	Thr	Leu	Leu	Tyr
	20								25				30		
Asp	Pro	Asp	Asn	Ala	Glu	Ala	Ile	Ala	Glu	Glu	Leu	Gly	Ala	Lys	Val
	35						40					45			
Ser	Lys	Phe	Leu	Arg											
	50														

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

Met Leu Trp Lys Tyr Tyr Asn Ser Ser Phe Leu Lys Ala Val Pro His
1 5 10 15
Leu Thr Thr Glu Tyr Lys Arg Leu Ala Gln Ala His Gly Leu Asn Leu
20 25 30
Lys Gln Ala Lys Pro Ile Thr Met Gly Met Trp Ile Gly Gly Asp Arg
35 40 45
Glu Gly Asn Pro Phe Val Thr Ala Lys Asn Leu Lys Gln Ser Ala Leu
50 55 60
Thr Gln Cys Glu Val Xaa Leu Asn Leu Leu
65 70

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

Met Asn Thr Leu Tyr Leu Asn Gln His Ser Ser Tyr Lys Asn Asp Glu
1 5 10 15
Asp Ser His Ser Phe Pro Ile Gln Met Glu Leu Val Ser Asp Glu Met
20 25 30
Ile Pro Arg Asn
35

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

Met Ala Arg Lys Glu Thr Met Ala Glu Arg Lys Tyr Cys Lys Met Lys
1 5 10 15
Lys Asp Ile His Pro Glu Tyr Arg Pro Val Val Phe Met Asp Thr Thr
20 25 30
Thr Gly Tyr Gln Phe Leu Ser Gly Ser Thr Lys Arg Ser Asn Glu Thr
35 40 45
Val Glu Phe Glu Gly Glu Thr Tyr Pro Leu Ile Arg Val Glu Ile Ser
50 55 60
Ser Asp Ser His Pro Phe Tyr Thr Gly Arg Gln Lys Phe Thr Gln Ala
65 70 75 80
Asp Gly Arg Val Asp Arg Phe Asn Lys Lys Tyr Gly Leu Lys
85 90

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

Met Glu Thr Ala Leu Ile Ser Val Ile Val Pro Val Tyr Asn Val Ala
1 5 10 15
Gln Tyr Leu Glu Lys Ser Ile Ala Ser Ile Gln Lys Gln Thr Tyr Gln
20 25 30
Asn Leu Glu Ile Ile Leu Val Asp Asp Gly Ala Thr Asp Glu Ser Gly
35 40 45
Arg Leu Cys Asp Ser Ile Ala Glu Gln Asp Asp Arg Val Ser Val Leu
50 55 60

His Lys Lys Asn Glu Gly Leu Ser Gln Ala Arg Asn Asp Gly Met Lys
65 70 75 80
Pro Gly Ser Arg Gly Leu Ser Asp Phe Tyr
85 90

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

Met Tyr Phe Leu Ile Asn Phe Val Tyr Pro Val Asp Met Val Ile Asn
1 5 10 15
Leu Pro Phe Leu Ile Asn Thr Gly Leu Ile Val Leu Leu Ser Ala Ile
20 25 30
Ser Tyr Ile Ser Leu Leu Val Phe Thr Lys Asp Ser Ile Phe Tyr Glu
35 40 45
Phe Leu Asn His Val Leu Ala Leu Lys Asn Lys Phe Lys Lys Ser
50 55 60

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

Met Arg Val Ile Ala Trp Leu Glu Pro Ser Arg Lys Ile Leu Gln Pro
1 5 10 15
Gly Ala Asn Asp Val Trp Val Val Lys Arg Lys Gly Lys Arg Asp Leu
20 25 30
Leu Leu Pro Tyr Ile Pro Pro Val Val Leu Asn Val Asp Ile Pro Asn
35 40 45

Lys Arg Val Asp Val Glu Ile Leu Glu Gly Leu Asp Asp Glu Asp
50 55 60

(2) INFORMATION FOR SEQ ID NO:436:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

Met Asp Asp Asp Phe Lys Arg Tyr Asn Ala Pro Ile Leu Thr Trp Tyr
1 5 10 15
Glu Thr Ala Arg Tyr Ala Phe Glu Arg Gly Met Val Trp Gln Asn Leu
20 25 30
Gly Gly Val Glu Asn Ser Leu Asn Gly Gly Leu Tyr His Phe Lys Glu
35 40 45
Lys Phe Asn Pro Thr Ile Glu Glu Tyr Leu Gly Glu Phe Thr Met Pro
50 55 60
Thr His Pro Leu Tyr Pro Leu Leu Arg Leu Ala Leu Asp Phe Arg Lys
65 70 75 80
Thr Leu Arg Lys Lys His Arg Lys
85

(2) INFORMATION FOR SEQ ID NO:437:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

Met Glu Asp Phe Phe Ala Trp Cys Arg Arg Gln Ser Val Leu Ser Gly
1 5 10 15
Ser Lys Leu Gly Arg Ala Ile Glu Tyr Ser Leu Lys Tyr Glu Glu Thr
20 25 30

Phe Lys Thr Ile Leu Lys Asp Gly His Leu Val Leu Ser Asn Asn Leu
35 40 45
Ala Glu Arg Ala Ile Lys Ser Leu Val Met Gly Arg Ser Lys Arg Val
50 55 60
Gln Trp Thr Leu Leu Ala
65 70

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

Met Thr Lys Gln Gly Ser Trp Lys Leu Ile Leu Glu Asp Glu Ser Ala
1 5 10 15
Gly Arg Glu Leu Phe Pro Ile Leu Thr Gln Gly Xaa Tyr Ile Ala Thr
20 25 30
Phe Asp Gln Gln Ala Pro Xaa Ile Asp Glu Ile Phe Lys Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

Met Thr Thr Asn Xaa Asp Asn Asp Thr Ser Glu Arg Ser Asp Cys Tyr
1 5 10 15
Arg Lys Arg Thr Ala Gly Glu Thr Pro Met Asn Asp Leu Thr Ser His
20 25 30
Thr His Gly Gly Asn Tyr Thr Ile Ala Arg Tyr Gln Glu Glu Lys Phe
35 40 45

Trp Asn Lys Gln Leu
50

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

Met Ala Gln His Ala Ala Val Glu Ala Leu Thr Ala Gly Lys Asn Asp
1 5 10 15
Ala Glu Pro Met Lys Lys Glu Tyr Ile Gln Arg Arg Asp Tyr Ile Ile
20 25 30
Glu Lys Met Thr Ala Leu Gly Phe Glu Ile Ile Lys Pro Asp Gly Ala
35 40 45
Phe Tyr Ile Phe Ala Lys Ile Pro Ala Gly Tyr Asn Gln Asp Ser Phe
50 55 60
Ala Phe Leu Lys Asp Phe Ala Gln Lys Lys Ala Val Ala Phe Ile Pro
65 70 75 80
Gly Ala Ala Phe Gly Arg Tyr Gly Glu Gly Tyr Val Arg Leu Ser Tyr
85 90 95
Ala Ala Ser Met Glu Thr Ile Lys Glu Ala Met Lys Arg Leu Glu Glu
100 105 110
Tyr Met Arg Glu Ala
115

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

Met Asn Ile Thr Asn Leu Phe Ser Ile Lys Thr Gly Cys Asp Glu Thr
 1 5 10 15
 Asp Arg Gln Leu Gln Lys Leu Phe Phe Gln Leu Asp Leu Gln Leu Gly
 20 25 30
 Glu Leu Thr Asp Gln Leu Arg Lys Leu Asp Ser Asn Phe Val Pro Arg
 35 40 45
 Ser Gln Phe Val Asp Thr Leu Asp Leu Asn Asp Val Glu Tyr Lys Glu
 50 55 60
 Ile Leu Asn Tyr Phe Ile Phe His Arg Asn Asp Ser Glu Glu Ser Leu
 65 70 75 80
 Val Glu Trp Leu Tyr Asp Trp Ile Ser Thr Asn Arg Tyr Glu Leu Pro
 85 90 95

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

Met Leu Gln Trp Ile Asp Arg Thr Phe Gln Asp Tyr Leu Glu Leu Glu
 1 5 10 15
 His Leu Val Leu Thr Thr Trp Ser Gly Asn Leu Gly Met Met Lys Leu
 20 25 30
 Ala Glu Lys Leu Xaa Met Lys Lys Xaa Ala His Ile Xaa Lys Val Arg
 35 40 45
 Tyr Tyr Gln Gly Lys Tyr Phe Asp Ser Ile Lys Tyr Gly Ile Leu Arg
 50 55 60
 Xaa Asp Trp Glu Lys Ile Asn Asp Gly Tyr Tyr Gln Ile Tyr Xaa Asn
 65 70 75 80
 Ser

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

Ser Ala Glu Lys Tyr Ala Lys Leu Gly Ile Glu Asn Leu Gln Asp Leu
20 25 30
Leu Leu Tyr Phe Pro Phe Arg Tyr Glu Asp Phe Lys Thr Lys Gln Val
35 40 45
Leu Glu Leu Glu Asp Gly Glu Lys Ala Val Leu Ser Gly Gln Val Val
50 55 60
Thr Pro Ala Ser Val Gln Tyr Tyr Gly Phe Gln Ala Ala Asn Pro Pro
65 70 75 80
Ala Phe Leu Val Leu Gln Ala Arg Glu Glu Gly Ser Phe Phe Gly
85 90 95
Gly

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

Met Gln Leu Leu Ser Glu Asn Met Leu Lys Thr Ile Gln Ser Leu Ser
1 5 10 15
Val Trp Gln Ile Tyr Leu Leu Gly Phe Glu Arg Ile Leu Ala Leu Gly
20 25 30
Phe Gln Leu Leu Thr Val Trp Val Tyr Gln Ala Val Arg Gln Lys
35 40 45
Lys Trp Ile Tyr Leu Leu Ala Ala Tyr Gly Leu His Ala Phe Phe Asp
50 55 60
Leu Ala Pro Ser Leu Phe Gln Val Gly Trp Leu Thr Asn Pro Val Leu
65 70 75 80
Val Glu Val Ile Leu Ala Leu Glu Leu Val Leu Val Ala Tyr Gly Thr
85 90 95
Lys Glu Ile Phe Cys Lys Lys Ser
100

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

Met Thr Lys Ser Met Thr Pro Asp Arg Glu Val Ile Thr Phe Ile Pro
1 5 10 15
Glu Lys Phe Ile Val Asp Gly Phe Gln Gly Ile Arg Asp Pro Arg Gly
20 25 30
Met Met Gly Val Arg Leu Glu Met Arg Gly Leu Leu Tyr Thr Gly Pro
35 40 45
Arg Thr Ile Leu His Asn Leu Arg Lys Thr Val Glu Arg Ala Gly Val
50 55 60
Gln Val Glu Asn Val Ile Ile Ser Pro Leu Ala Met Val Gln Ser Val
65 70 75 80
Leu Asn Glu Gly Glu Arg Glu Phe Gly Ala Thr Val Ile Asp Met Gly
85 90 95
Ala Gly Gln Thr Thr Val Ala Thr Ile Arg Asn Gln Glu Leu Gln Phe
100 105 110
Thr His Ile Leu Gln Glu Val Glu Ile Met
115 120

(2) INFORMATION FOR SEQ ID NO:447:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

Met Leu Asn Ser Ile Val Thr Ile Ile Cys Ile Ala Leu Ile Ala Phe
1 5 10 15
Ile Leu Phe Trp Phe Phe Lys Lys Pro Glu Lys Ser Gly Gln Lys Ala
20 25 30
Gln Gln Lys Asn Gly Tyr Gln Glu Ile Arg Val Glu Val Met Gly Gly
35 40 45

Tyr Thr Pro Glu Leu Ile Val Leu Lys Lys Ser Val Pro Ala Arg Ile
50 55 60
Val Phe Asp Arg Lys Asp Pro Ser Pro Cys Leu Asp Gln Ile Val Phe
65 70 75 80
Pro Asp Phe Gly Val His Ala Asn Leu Pro Met Gly Glu Glu Tyr Val
85 90 95
Val Glu Ile Thr Pro Glu Gln Ala Gly Glu Phe Gly Phe Ala Cys Gly
100 105 110
Met Asn Met Met His Gly Lys Met Ile Val Glu
115 120

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

Met Lys Ile Val Ser Gly Ile Tyr Gly Gly Arg Pro Leu Lys Thr Leu
1 5 10 15
Glu Gly Lys Thr Thr Arg Pro Thr Ser Asp Lys Val Arg Gly Ala Ile
20 25 30
Phe Asn Met Ile Gly Pro Tyr Phe Glu Val Gly Xaa Val Leu Asp Leu
35 40 45
Tyr Ala Gly Ser Gly Gly Leu Ser Ile Glu Ala Val Ser Arg Gly Met
50 55 60
Ser Ser Ala Val Leu Val Glu Arg Asp Arg Lys Ala Gln Thr Ile Val
65 70 75 80
Ala Glu Asn Ile Gln Met Thr Lys Glu Val Gly Lys Phe Gln Leu Leu
85 90 95
Gln Asn Gly Cys Arg Lys Gly Ile Gly Thr Gly Xaa Leu Gly Asn Leu
100 105 110
Thr Ser Phe Ser
115

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

Met Xaa Thr Asn Phe Thr Asp Gln Val Asp Thr Met Ile Tyr Val Asp
1 5 10 15
Lys Glu Glu Lys Glu Thr Ile Lys Ala Ala Leu Val Glu Phe Phe Asn
20 25 30
Gly Lys Val Thr Leu Thr Asp Gln Gly Leu Arg Glu Val Glu Val Pro
35 40 45
Val Asn Leu Val
50

(2) INFORMATION FOR SEQ ID NO:450:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

Met Ile Gly Val Ala Leu Glu Glu Ser Pro Thr Leu Lys Ile His His
1 5 10 15
Leu Thr His Asp Ile Thr Pro Tyr Asn Ile Phe Glu Gly Ser Tyr Arg
20 25 30
Leu Phe Gln Thr Val Asp Tyr Trp Pro Glu Gly Thr Thr Phe Val Ser
35 40 45
Val Val Asp Pro Gly Val Gly Ser Lys Arg Lys Ser Val Val Ala Lys
50 55 60
Thr Ala Gln Lys Ser Ile His Cys His Ala Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:451:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 130 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

Met Glu Leu Arg Arg Pro Arg Leu Ala Asp Lys Lys Ala Val Leu Asp
1 5 10 15
Met Met Thr Glu Phe Glu Lys Ser Gln Ser Ala His Asp Gly Gly Phe
20 25 30
Trp Asp Thr Glu Asn Phe Val Tyr Glu Glu Trp Leu Glu Ser Asn Gln
35 40 45
Glu Gln Glu Met Gly Ile Asn Leu Pro Glu Gly Trp Val Pro Ala Ile
50 55 60
Gln Leu Val Ala Phe Ser Glu Lys Gly Gln Ala Val Gly Phe Leu Asn
65 70 75 80
Leu Arg Leu Arg Leu Ser Asn Phe Leu Leu Glu Glu Gly His Ile
85 90 95
Gly Tyr Ser Ile Arg Pro Ser Glu Arg Gly Lys Gly Tyr Ala Lys Glu
100 105 110
Leu Ser Val Arg Ala Cys Lys Leu Leu Arg Lys Arg Thr Ser Arg Lys
115 120 125
Leu Trp
130

(2) INFORMATION FOR SEQ ID NO:452:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

Met Thr Phe Ile Arg Gly Pro Ile Ile Ser Thr Val Gly Glu Gly Val
1 5 10 15
Xaa Ile Leu Ala Thr Val Asn Xaa Gln Phe Val Xaa Xaa Gln Xaa Xaa
20 25 30

Asn Met Leu Val Ser Pro Phe His Pro Glu Leu Thr Asp Xaa Xaa Arg
35 40 45
Leu Xaa Gln Tyr Phe Ile Ser Met Cys Lys Glu Lys Ser Xaa Asp
50 55 60

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

Met Lys Gly Asp Val Ile Thr Glu His Gln Phe Tyr Glu Gln Val Lys
1 5 10 15
Asn Asn Pro Ser Ala Gln Xaa Val Leu Leu Asn Met Thr Ile Gln Lys
20 25 30
Val Phe Glu Lys Thr Ile Trp Leu Arg Ala
35 40

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

Met Asp Lys Ala Leu Ala Asp Leu Lys Thr Ser Gly His Leu Pro Ile
1 5 10 15
Pro Arg His Leu Arg Asp Gly His Tyr Xaa Gly Ser Lys Glu Leu Gly
20 25 30
Asn Ala Gln Asp Tyr Leu Tyr Pro His Asn Tyr Pro Xaa Asn Trp Val
35 40 45
Lys Gln Asp Tyr Leu Pro Gln Lys Ile Arg Asn His His Tyr Phe Gln
50 55 60

WO 97/37026

Ala Glu Tyr Thr Gly Lys Tyr Glu Arg Ala Leu Ala Gln Arg Lys Glu			
65	70	75	80
Ala Ile Asp His Leu Arg Lys Ile			
85			

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

Met Val Val Phe Thr Gly Ser Thr Val Glu Glu Ala Ile Gln Lys Gly			
1	5	10	15
Leu Lys Glu Leu Asp Ile Pro Arg Met Lys Ala His Ile Lys Val Ile			
20	25	30	
Ser Arg Glu Lys Lys Gly Phe Leu Gly Leu Phe Gly Lys Lys Pro Ala			
35	40	45	
Gln Val Asp Ile Glu Ala Ile Ser Glu Thr Thr Val Val Lys Ala Asn			
50	55	60	
Gln Gln Val Val Lys Gly Val Pro Lys Lys Ile Asn Asp Leu Asn Glu			
65	70	75	80
Pro Val Lys Thr Val Ser Val Arg Asn Arg			
85	90		

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

Met Thr Lys Arg Cys Ser Trp Val Lys Met Thr Asn Pro Leu Tyr Ile			
1	5	10	15

Ala Tyr His Asp Glu Glu Trp Gly Gln Pro Leu His Asp Asp Gln Ala
20 25 30
Leu Phe Glu Leu Leu Cys Met Glu Thr Tyr Tyr Gln Ala Gly Leu Ser Trp
35 40 45
Glu Thr Val Leu Asn Lys Arg Gln Ala Phe Arg Glu Ala Phe Pro
50 55 60

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

Met Phe Val Gly Gln Glu Trp Thr Asn Gln Thr Phe Val Asp Leu Leu
1 5 10 15
Gly Asn His Gln Gln Gly Val Thr Ile Asp Glu Glu Gly Tyr Gly Gln
20 25 30
Phe Pro Val Ser Ala Arg Ser Val Ser Val Trp Ala Val Asn Thr Ile
35 40 45

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

Met Ala Gln Val Asp Ile Ile His Gly Ile Gly Thr Gly Val Ile Arg
1 5 10 15
Glu Gly Val Thr Lys Tyr Leu Gln Arg Asn Lys His Val Lys Ser Phe
20 25 30
Gly Tyr Ala Pro Gln Asn Ala Gly Gly Ser Gly Ala Thr Ile Val Thr
35 40 45

Phe Lys Gly
50

(2) INFORMATION FOR SEQ ID NO:459:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

Met Asn Leu Leu Glu Glu Ala Thr Lys Gly Lys Val Ile Phe Glu Gly
1 5 10 15
Val Asp Ile Thr Asp Lys Lys Asn Asp Leu Phe Pro Met Arg Glu Lys
20 25 30
Met Gly Met Val Phe Gln Gln Phe Asn Xaa Phe Leu Ile
35 40 45

(2) INFORMATION FOR SEQ ID NO:460:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

Met Gln Ile Asp Leu Ala Asn Leu Leu Pro Asp Leu Pro Gly Asn Leu
1 5 10 15
Ser Gly Ile Asn Pro Asn Arg Tyr Val Phe Tyr Gln Asp Val Leu Cys
20 25 30
Pro Ile Leu Asp Arg His Met Thr Pro Glu Gln Asp Lys Pro His Phe
35 40 45
Ala Gln Ala Ala Gly Thr Ile Ala Asp Ile Lys Glu Lys Ala Gly Asn
50 55 60
Tyr Ala Tyr Leu Phe Glu Thr Gln Ala Gln Leu Asn Ala Ile Leu Ser
65 70 75 80

Ser Lys Val Asp Val Gly Arg Arg Ile Arg His Ala Tyr Gln Ala Asp
85 90 95
Asp Lys Glu Ser Leu Gln Gln Ile Ala Arg Gln Glu Leu Pro Glu Leu
100 105 110.
Arg Ser Gln Ile Glu Asp Phe His Ala Leu Phe Ser His His Trp Leu
115 120 125
Lys

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

Met Arg Gln Gly Ile Asp Ser Leu Ala Tyr Val Val Lys Thr His Phe
1 5 10 15
Glu Leu Asp Pro Phe Ser Gly Gln Ala Phe Leu Phe Cys Gly Gly Arg
20 25 30
Lys Asp Arg Phe Lys Ala Leu Tyr Trp Asp Gly Gln Gly Phe Trp Leu
35 40 45
Leu Tyr Lys Arg Phe Glu Asn Gly Lys Leu Thr
50 55

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

Met Asn Ala Phe Leu Glu Glu Leu Ser Gln Ala Tyr Pro Asp Asp Tyr
1 5 10 15

Phe	Leu	Leu	Val	Met	Asp	Asn	Ala	Ile	Trp	His	Lys	Ser	Ser	Val	Leu
20								25						30	
Lys	Ile	Pro	Thr	Asn	Ile	Gly	Phe	Ala	Phe	Ile	Pro	Pro	Tyr	Thr	Pro
35								40					45		
Glu	Met	Asn	Pro	Ile	Glu	Gln	Val	Trp	Lys	Glu	Ile	Arg	Lys	Arg	Gly
50							55				60				
Phe	Lys	Asn	Lys	Ala	Phe	Arg	Ile	Leu	Glu	Asp	Val	Met	Asn	Gln	Leu
65							70			75			80		
Gln	Asp	Val	Ile	Gln	Gly	Leu	Glu	Lys	Glu	Val	Ile	Lys	Ser	Ile	Val
85							90						95		
Asn	Arg	Arg	Trp	Thr	Arg	Met	Leu	Phe	Glu	Ser	Arg				
100							105								

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

Met	Thr	Val	Glu	Glu	Glu	Lys	Val	Phe	Leu	Ala	Arg	His	Lys	Ala	
1			5						10				15		
Thr	Glu	Ala	Gly	Glu	Phe	Val	Thr	Ile	Asp	Ala	Leu	Phe	Gln	Ala	Tyr
							20				25		30		
Lys	Lys	Glu	Leu	Gly	Arg	Ser	Tyr	Thr	Arg	Asp	Ala	Phe	Tyr	Gln	Leu
						35			40				45		
Leu	Lys	Arg	His	Gly	Trp	Arg	Asn	Ile	Met	Pro	Arg	Pro	Glu	His	Pro
							50		55			60			
Lys	Lys	Ala	Asp	Ala	Gln	Thr	Ile	Val	Ala	Ser	Lys	Asn	Lys	Ile	Ser
							65		70		75		80		
Ile	Gln	Glu	Asp	Lys	Lys	Ala	Ile								
							85								

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

Met Leu Ser Leu Val Val Leu Ile Thr Gln Tyr Ala Thr His Gly Glu
1 5 10 15
Leu Phe Glu Asn Tyr Ile Ser Lys Glu Asn Asp Asn Val Ile Lys Glu
20 25 30
Tyr Gln Asn Thr Thr Gly Phe Ser Thr Pro Tyr Thr Leu Asp Gly Ser
35 40 45
Val Leu Ile Val His Pro Asp Leu Thr Lys Gly Met Asn Ile Glu Gly
50 55 60
Tyr Ser Asp Leu Leu Lys Pro Glu Leu Lys Gly Lys Ile Ala Thr Ala
65 70 75 80
Asp Pro Ala Asn Ser Ser Ala Phe Ala Gln Leu Thr Asn Met Leu
85 90 95
Gln Ala Gln Gly Gly Tyr Lys Asp Asp Leu Ala Trp Ser Val Leu Ser
100 105 110
Thr Ile Phe Ser Thr Leu Ile Asp Gly Ile Val Lys
115 120

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

Met Leu Ala Arg Lys Asp Arg Phe Tyr Tyr Ile Asp Lys Ala Thr Gly
1 5 10 15
Lys Ala Leu Gly Ile Phe Leu Ser Cys Val Leu Thr Ser Asn Gly Val
20 25 30
Ile Glu Val Gly Ala Val Thr Phe Ser Pro Lys Leu Arg Gly Thr Arg
35 40 45

Ile Gly Thr Glu Ala Gln Tyr Leu Leu Ala Arg Tyr Val Phe Glu Glu
50 55 60
Leu Asn Tyr Arg Arg Tyr Glu Trp Lys Cys Asp Ala Leu Asn Leu Pro
65 70 75 80
Ser Arg Arg Ala Ala Glu Arg Leu Gly Phe Ile Tyr Glu Gly Thr Phe
85 90 95
Arg Gln Ala Val Val Tyr Lys Gly Arg Thr Arg Asp Met Asp Trp Leu
100 105 110
Ser Met Ile Asp Lys Asp Trp Pro Lys Val Lys Asp Arg Leu Glu Thr
115 120 125
Trp Leu Arg Pro Glu Asn Phe Asp Lys Asn Gly Gln Gln Tyr Lys Ser
130 135 140
Leu Arg Glu Leu
145

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

Met Met Thr Ser Asp Phe Phe Glu Val Trp Phe Gln Lys Phe Leu Leu
1 5 10 15
Pro Thr Leu Thr Thr Pro Ser Val Ile Ile Val Lys
20 25

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

Met Val Ser Thr Lys Thr Gln Ile Ala Gly Phe Glu Phe Asp Asn Cys
1 5 10 15
Leu Met Asn Ala Ala Gly Val Ala Cys Met Thr Ile Glu Glu Leu Glu
20 25 30
Glu Val Lys Asn Ser Ala Ala Gly Thr Phe Val Thr Lys Thr Ala Thr
35 40 45
Leu Asp Phe Arg Gln Gly Asn Pro Glu Pro Arg Tyr Gln Asp Val Pro
50 55 60
Leu Gly Ser Ile Asn Ser Met Gly Leu Pro Asn Asn Gly Leu Asp Tyr
65 70 75 80
Tyr Leu Asp Tyr Leu Leu Asp Leu Gln Glu Lys Glu Ser Asn Arg Thr
85 90 95
Phe Phe Leu Ser Leu Val Gly Met Ser Pro Glu Lys Pro Ile Leu Phe
100 105 110

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

Met Thr Tyr Leu Met Phe Ser Gly Leu Asp Asn Phe Tyr His Phe
1 5 10 15
Pro Trp Glu Val Phe Ala Gly Phe Gly Ile Ile Phe Leu Ala Cys Pro
20 25 30
Glu Lys Val
35

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

Met Phe Thr Gly Trp Phe Ala Gln Thr Phe Leu His Gln Phe Ile Arg
1 5 10 15
Gly Ala Trp Gly Leu Gly Phe Met Ile Phe Ile Ala Phe Pro Met Gly
20 25 30
Lys Glu Leu Leu Glu Gly Glu Tyr His Glu His Asp
35 40

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

Met Gln Glu Lys Ile Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Thr
1 5 10 15
His Thr Val Ile Glu Leu Ile Gln Ala Gly His Gln Val Val Val Val
20 25 30
Asp Asn Leu Val Asn Ser Asn Xaa Lys Ser Leu Glu Val Val Glu Arg
35 40 45
Ile Thr Gly Val Glu Ile Pro Phe Tyr Glu Ala Asp Ile Xaa Asp Thr
50 55 60
Asp Thr Leu Arg Asp Ile Phe Lys Gln Glu Glu Leu Thr Gly Val Ile
65 70 75 80
His Phe Ala Gly Leu Lys Ala Val Gly Glu Ser Thr Arg Ile Pro Leu
85 90 95
Ala Tyr Tyr Asp Asn Asn Ile Ala Gly Thr Val Ser Leu Leu Lys Ala
100 105 110
Met Glu Glu Asn Asn Cys Lys Asn Ile Ile Phe Ser Ser Xaa Ala Thr
115 120 125
Val Tyr Gly Asp Pro Tyr Thr Val Pro Ile Leu Glu Val Ser His Phe
130 135 140
Gln
145

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

Met	Val	Lys	Glu	Lys	Val	Thr	Leu	Thr	Pro	Leu	Ala	Ser	Gly	Tyr	Gln
1					5				10					15	
Ile	Gly	Glu	Glu	Glu	Phe	Glu	Gln	Val	Ile	Leu	Ala	Xaa	Gly	Ala	Trp
					20				25					30	
Leu	Gly	Asp	Met	Leu	Glu	Pro	Leu	Gly	Tyr	Glu	Val	Asp	Val	Arg	Pro
			35				40					45			
Gln	Lys	Gly	Gln	Leu	Arg	Asp	Tyr	Gln	Leu	Val	Gln	Asp	Met	Glu	Ala
			50				55				60				
Tyr	Pro	Val	Val	Met	Pro	Glu	Gly	Trp	Asp	Leu	Ile	Pro	Phe	Ala	
	65					70				75			80		
Gly	Gly	Lys	Leu	Ser	Leu	Gly	Ala	Thr	His	Glu	Asn	Asp	Met	Gly	Phe
						85				90			95		
Asp	Leu	Thr	Val	Asp	Glu	Thr	Leu	Leu	Gln	Met	Glu	Glu	Ala	Thr	
				100				105				110			
Leu	Thr	His	Tyr	Leu	Ile	Leu	Ala	Glu	Ala	Thr	Ser	Lys	Ser	Glu	Arg
				115				120				125			
Val	Gly	Ile	Arg	Ala	Tyr	Thr	Ser	Asp	Phe	Ser	Pro	Phe	Phe	Gln	
				130				135				140			
Val	Pro	Asp	Leu	Thr	Gly	Val	Tyr	Ala	Ala	Ser	Gly	Leu	Gly	Ser	Ser
	145					150				155			160		
Gly	Leu	Thr	Thr	Gly	Pro	Ile	Ile	Gly	Tyr	His	Leu	Ala	Gln	Leu	Ile
					165				170				175		
Gln	Asp	Lys	Glu	Leu	Thr	Leu	Asp	Pro	Glu	Asn	Tyr	Pro	Ile	Glu	Asn
					180				185			190			
Tyr	Val	Lys	Arg	Val	Lys	Ser	Glu								
				195				200							

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

Met Glu His Ile Ile Tyr Gln Phe Glu Glu Asp Leu Ala Ile Leu Thr
1 5 10 15
Leu Asn Arg Pro Glu Val Ala Asn Gly Phe His Ile Pro Met Cys Glu
20 25 30
Glu Ile Leu Glu Ala Leu Thr Leu Ala Glu Glu Asn Pro Ala Val His
35 40 45
Phe Ile Leu Ile Asn Ala Asn Gly Lys Val Phe Ser Val Gly Gly Asp
50 55 60
Leu Val Glu Met Lys Arg Ala Val Asp Glu Asp Asp Ile Pro Ser Leu
65 70 75 80
Thr Lys Ile Ala Glu Leu Val Asn Thr Ile Ser Tyr Lys Ile Lys Gln
85 90 95
Ile Ala Lys Pro Val Phe Asn Gly Ser
100 105

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

Met Gln Pro Glu Val Ile Trp Leu Gln Lys Ile Ala Lys Pro Ser Gln
1 5 10 15
Met Lys Val Leu Asn Thr Thr Asp Arg Val Gln Ala Ile Lys Asp Asp
20 25 30
Val Asp Ile Ile Gln Asn Ser Leu Gln Ile Ile Asn Gln Gln Lys Glu
35 40 45
Leu Ile Lys Glu Tyr Gln Glu Asp Leu Thr Tyr Lys Phe Lys Val Leu
50 55 60
Glu Lys Asp Ile Gln Thr Arg Thr Ser Cys Asp Lys Arg Asn Ala Gly
65 70 75 80
Asn

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

Met	Gly	Ser	Asn	Ser	Leu	Thr	Leu	Leu	Lys	Ile	Gln	Ala	Thr	Ile	
1					5				10				15		
Pro	Arg	Asn	Ile	Tyr	Asp	Asn	Leu	Gln	Ala	Gly	Ser	Lys	Val	Thr	Leu
									20			25		30	
Asp	Arg	Ala	Tyr	Gly	His	Met	Ile	Ile	Glu	Glu	Gly	Arg	Glu	Asn	Gln
						35			40			45			
Val	Trp	Ile	Ala	Gly	Gly	Ile	Gly	Ile	Thr	Pro	Phe	Ile	Ser	Tyr	Ile
						50			55			60			
Arg	Glu	His	Pro	Ile	Leu	Asp	Lys	Gln	Val	His	Phe	Tyr	Tyr	Ser	Phe
						65			70			75		80	
Arg	Gly	Asp	Glu	Asn	Ala	Val	Tyr	Leu	Asp	Leu	Leu	Arg	Asn	Tyr	Ala
						85			90			95			
Gln	Lys	Asn	Pro	Asn	Phe	Glu	Leu	His	Leu	Ile	Asp	Ser	Thr	Lys	Asp
						100			105			110			
Gly	Tyr	Leu	Asn	Phe	Glu	Gln	Lys	Lys	Cys	Pro	Asn	Met	Gln	Pro	Ser
						115			120			125			
Ile	Cys	Val	Val	Leu	Phe	Leu									
						130									
															135

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

Met Phe Phe Val Leu Ala Tyr Ala Lys Ala Val Ala Gly Arg Asn Ile
1 5 10 15
Lys Leu His Pro Ile Gln Arg Gln Gly Ala Gly Tyr His Ser Val Asn
20 25 30
Lys Asp Val Asp Phe Ala Ser Ala Thr Ala Leu Arg Gln His Gln Lys
35 40 45
Asp Gln Asp Phe Leu Glu Arg Phe Met Pro Ser Val Ala Leu Phe Glu
50 55 60
Gln Ala Ser Lys Val Ile Trp Glu Asp Tyr Phe Pro Leu Leu Arg Tyr
65 70 75 80
Gln Ile Leu Ser Asn Pro Asp Leu Thr Thr Ile Tyr Gln Val Asn Gln
85 90 95
Glu Met Ala Val Arg Ile Lys Glu Ala Ile Lys Thr Ala Gln Ser Val
100 105 110
Glu Glu Leu Val Glu Leu Val Thr Thr Lys Arg Tyr Thr Lys Ala Arg
115 120 125
Val Arg Arg Leu Leu Thr Tyr Ile Leu Met Gln Ala Arg Glu Ser Asp
130 135 140
Leu Pro Glu Ala Ile His Val Leu Gly Phe Thr Glu Lys Gly Arg Gln
145 150 155 160
His Leu Lys Ser Leu Lys Gly Gln Val Asn Leu Val Ser Arg Ile Gly
165 170 175
Lys Glu Pro Trp Asp Ala Met Thr Gln Lys Val Asp Gln Ile Tyr Gln
180 185 190
Leu Gly Lys Pro Ser Ile Ala Glu Gln Asn Phe Gly Arg Val Pro Ile
195 200 205
Arg Ile Glu Thr Asn
210

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

Met Leu Gly Ser Met Phe Val Gly Leu Leu Val Gly Phe Leu Ala Gly
1 5 10 15

Ala Met Thr Asn Arg Gly Glu Arg Met Gly Cys Phe Gly Lys Met Phe
20 25 30
Leu Gly Trp Ile Gly Ala Phe Leu Gly His Leu Leu Phe Gly Thr Trp
35 40 45
Gly Pro Val Leu Ser Gly Thr Ala Ile Ile Pro Ala Val Leu Gly Ala
50 55 60
Met Ile Val Leu Ala Ile Phe Trp Arg Arg Gly Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

Met Arg Ser Ser Pro Ser Arg Glu Ile Gln Pro Arg Ser Trp Gly Ile
1 5 10 15
Thr Thr Val Tyr Val Thr His Asp Gln Glu Gly Ala Met Ala Ile Ser
20 25 30
Asp Gln Ile Ala Cys Tyr Glu Arg Trp Gly Asp Pro Thr Asn Arg Pro
35 40 45
Thr Lys Arg Thr Val Ser
50

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:
 - 5 (a) a polynucleotide having at least a 70% identity to a polynucleotide encoding a polypeptide comprising an amino acid sequence of selected from the group consisting of SEQ ID NO:224 through 477,
 - (b) a polynucleotide which is complementary to the polynucleotide of (a);
 - (c) a polynucleotide having at least a 70% identity to a polynucleotide encoding the same mature polypeptide expressed by the gene comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1 through 223 contained in the DNA of the deposited clone; and
 - (d) a polynucleotide comprising at least 15 sequential bases of the polynucleotide of (a), (b) or (c).
 - 15 2. The polynucleotide of Claim 1 wherein the polynucleotide is DNA.
 3. The polynucleotide of Claim 1 wherein the polynucleotide is RNA.
 4. The polynucleotide of Claim 2 comprising the nucleic acid sequence set forth in SEQ ID NO:1.
 5. The polynucleotide of Claim 2 comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1 through 223.
 - 20 6. The polynucleotide of Claim 2 which encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:224 through 477.
 7. A vector comprising the polynucleotide of Claim 1.
 8. A host cell comprising the vector of Claim 7.
 - 25 9. A process for producing a polypeptide comprising: expressing from the host cell of Claim 8 a polypeptide encoded by said DNA.
 10. A process for producing a novel polypeptide or fragment comprising culturing a host of claim 8 under conditions sufficient for the production of said polypeptide or fragment.
 - 30 11. A polypeptide comprising an amino acid sequence which is at least 70% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:224 through 477.
 12. A polypeptide comprising an amino acid selected from the group consisting of SEQ ID NO:224 through 477.

13. An antibody against the polypeptide of claim 11.
14. An antagonist which inhibits the activity or expression of the polypeptide of claim 11.
15. A method for the treatment of an individual in need of a Streptococcal polypeptide comprising: administering to the individual a therapeutically effective amount of the polypeptide of claim 11.
- 5 16. A method for the treatment of an individual having need to inhibit a bacterial polypeptide comprising: administering to the individual a therapeutically effective amount of the antagonist of Claim 14.
- 10 17. A process for diagnosing a disease related to expression or activity of the polypeptide of claim 11 in an individual comprising:
 - (a) determining a nucleic acid sequence encoding said polypeptide, and/or
 - (b) analyzing for the presence or amount of said polypeptide in a sample derived from the individual.
- 15 18. A method for identifying compounds which interact with and inhibit or activate an activity of the polypeptide of claim 11 comprising:
 - contacting a composition comprising the polypeptide with the compound to be screened under conditions to permit interaction between the compound and the polypeptide to assess the interaction of a compound, such interaction being associated with a second component capable of
 - 20 providing a detectable signal in response to the interaction of the polypeptide with the compound;

and determining whether the compound interacts with and activates or inhibits an activity of the polypeptide by detecting the presence or absence of a signal generated from the interaction of the compound with the polypeptide.
- 25 19. A method for inducing an immunological response in a mammal which comprises inoculating the mammal with Streptococcal polypeptide of claim 11, or a fragment or variant thereof, adequate to produce antibody and/or T cell immune response to protect said animal from disease.
- 30 20. A method of inducing immunological response in a mammal which comprises delivering a nucleic acid vector to direct expression of Streptococcal polypeptide of claim 11, or fragment or a variant thereof, for expressing said Streptococcal polypeptide, or a fragment or a variant thereof *in vivo* in order to induce an immunological response to produce antibody and/or T cell immune response to protect said animal from disease.

21. An isolated Streptococcal polypeptide having one of the amino acid sequences of SEQ ID NO:224 through SEQ ID NO:234.
22. An isolated nucleic acid encoding one of the amino acid sequences of Claim 21 and nucleic acid sequences capable of hybridizing therewith under stringent conditions.
23. Recombinant vectors comprising the nucleic acid sequences of Claim 22 and host cells transformed or transfected therewith.
24. A method of identifying an antimicrobial compound comprising contacting candidate compounds with a polypeptide of Claim 21 and selecting those compounds capable of inhibiting the bioactivity of said polypeptide.
- 10 25. Antimicrobial compounds identified by the method of Claim 24.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US97/05306

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :Please See Extra Sheet.

US CL :536/23.7; 435/6, 69.1, 252.3, 320.1; 530/324, 350; 514/12

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.7; 435/6, 69.1, 252.3, 320.1; 530/324, 350; 514/12

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X, P ---	WO 96/10647 A1 (FUSO PHARMACEUTICAL INDUSTRIES, LTD.) 11 April 1996, claim 2, pages 22-24.	1, 2, 7, 8, and 22
Y, P		----- 3, 6, 9-12, 15, 17, 21, and 23-25
Y	WATSON, J. D. et al. Recombinant DNA, Second Edition. New York: Scientific American Books, W.H. Freeman and Company, 1992, pages 73 and 74, see entire document.	1-3, 6-12, 15, 17, and 21-23
Y	KENNELL, D. E. Principles and Practices of Nucleic Acid Hybridization. Progress in Nucleic Acid Research Molecular Biology. 1971, Vol. 11, pages 259-301, see especially pages 259-262.	1-3, 6-12, 15, 17, and 21-23

 Further documents are listed in the continuation of Box C. See patent family annex.

* Special categories of cited documents:	"T"	later documents published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"		document defining the general state of the art which is not considered to be of particular relevance
"B"	"X"	earlier documents published on or after the international filing date
"L"		document which may throw doubt on priority claim(s) or which is cited to establish the publication date of another citation or other special reasons (as specified)
"O"	"Y"	document referring to an oral disclosure, use, exhibition or other means
"P"	"Z"	documents published prior to the international filing date but later than the priority date claimed

Date of the actual completion of the international search

10 JULY 1997

Date of mailing of the international search report

06 AUG 1997

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
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Authorized officer

JAMES MARTINELL

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INTERNATIONAL SEARCH REPORT

International application No. PCT/US97/05306

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:

2. Claims Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-3, 6-12, 15, 17, and 21-23 (SEQ ID NOS 224-233).

Remark on Protest

- The additional search fees were accompanied by the applicant's protest.
 No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORTInternational application No.
PCT/US97/05306**BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING (Continued):**

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I. Claims 1-12, 15, 17, and 21-23, drawn to nucleic acids and polypeptides of specific sequence, vectors containing nucleic acids, methods of producing polypeptides, and methods of treatment using polypeptides.

Group II. Claims 13 and 19, drawn to antibodies against any of no fewer than 254 specific sequence polypeptides.

Group III. Claims 14 and 16, drawn to antagonists of undisclosed composition of the activity of no fewer than 254 specific sequence polypeptides.

Group IV. Claims 18 and 24, drawn to methods for screening for compounds that interact with no fewer than 254 specific sequence polypeptides.

Group V. Claim 20, drawn to a method of inducing an immunological response using a nucleic acid.

Group VI. Claim 25, drawn to compounds of undisclosed composition.

The inventions listed as Groups I-VI do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons. The nucleic acids, proteins, and methods of Group I are materially different from the antibodies of Group II, the compounds of Group III, and the compounds of Group VI and are not required to produce either the antibodies of Group II, which antibodies may be made with antigens other than those embraced by Group I. Additionally, the methods of Group I are not needed to produce the compounds of either one of Groups III or VI. The compositions and methods of Group I are not needed for the methods of either one of Groups IV or V. The antibodies of Group II are not needed for the methods of Groups IV or V and are materially different from the compounds of Groups III and VI. The antagonists of Group III are materially different from the compounds of Group VI because the antagonists and compounds have differing sites of action and/or binding. Neither are the compounds of either one of Groups III or VI needed to practice the methods of either one of Groups IV or V. The methods of Groups IV and V may be practiced independently of one another.

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack Unity of Invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows. Each of the 234 SEQ ID NOs listed is a separate species because there is no relationship between the species.

The species listed above do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, the species lack the same or corresponding special technical features for the following reasons. There is no relationship among the species.

For any Group applicant elects, a total of 10 (TEN) specified sequences will be searched and no more than 4 (FOUR) specified sequences will be searched for each additional fee paid.

The claims are deemed to correspond to the species listed above in the following manner: SEQ ID NOs 224-233 correspond to claims 1-3, 6-12, 15, 17, and 21-23.

A. CLASSIFICATION OF SUBJECT MATTER:

IPC (6):

C12N 15/31, 15/11, 15/00; C12P 21/02; A61K 38/16, 39/09; C07K 14/195, 14/315

B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

MPSRCH OF: A-GENESEQ26, A-ISSUED, HIV-AA2, PIR50, SUTWW-PROT34, EMBL-NEW11, GENBANK97, GENBANK-NEW11, U-EMBL48_97, HIV-NA8, N-GENESEQ26, N-ISSUED, EST-STS, EST-STS-TWO, EST-STS-

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/05306

THREE. SEQ ID NOs 224-233.